```
 * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * *
FILE 'HOME' ENTERED AT 14:41:39 ON 15 JUN 2004
=> file biosis,caba,caplus,embase,japio,lifesci,medline,scisearch,uspatfull
=> E KEIM PAUL S/AU
E1            1     KEIM PATRICIA/AU
E2          178     KEIM PAUL/AU
E3            5 --> KEIM PAUL S/AU
E4            2     KEIM PAUL STEPHEN/AU
E5            6     KEIM PETER/AU
E6            3     KEIM PETER C/AU
E7           16     KEIM PHILIP/AU
E8            1     KEIM PIET M/AU
E9           57     KEIM R/AU
E10           3     KEIM R E/AU
E11          12     KEIM R F/AU
E12          24     KEIM R G/AU

=> s e2-e4 and tubercul?
L1            3 ("KEIM PAUL"/AU OR "KEIM PAUL S"/AU OR "KEIM PAUL STEPHEN"/AU)
                AND TUBERCUL?

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2            2 DUP REM L1 (1 DUPLICATE REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 2 ANSWERS - CONTINUE? Y/(N):y

L2   ANSWER 1 OF 2  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2004:80897  CAPLUS
DN   140:140628
TI   Primers and kits for genotyping Mycobacterium   ***tuberculosis***
     strains by detecting variable-number tandem repeat loci
IN     ***Keim, Paul S.***  ; Schupp, James M.; Spurgiesz, Robert Scott
PA   Arizona Board of Regents, USA
SO   PCT Int. Appl., 44 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.         KIND  DATE           APPLICATION NO.  DATE
     ---------------    ----  --------       ---------------  --------
PI   WO 2004009837      A2    20040129       WO 2003-US22950  20030721
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM,
             PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN,
             TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG,
             KZ, MD, RU, TJ
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
             CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC,
             NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
             GW, ML, MR, NE, SN, TD, TG
PRAI US 2002-397224P   P    20020719
AB   MLVA methods for strain discrimination among Mycobacterium
       ***tuberculosum***   strains are disclosed. Nine VNTR loci have been
     identified from genomic sequences of Mycobacterium   ***tuberculosum***
     strains and primer pairs suitable for amplifying the VNTR by PCR are
     disclosed. Polymorphisms at these loci were used to resolve genotypes
     into distinct groups. This sub-typing scheme is useful for the epidemiol.
     study of Mycobacterium   ***tuberculosum***   and may be applied to the
     local detection of the pathol. causative agent of   ***tuberculosum***   .

L2   ANSWER 2 OF 2  CAPLUS  COPYRIGHT 2004 ACS on STN  DUPLICATE 1
AN   2003:792964  CAPLUS
DN   140:23719
TI   Molecular typing of Mycobacterium   ***tuberculosis***   by using nine
     novel variable-number tandem repeats across the Beijing family and
     low-copy-number IS6110 isolates
AU   Spurgiesz, R. Scott; Quitugua, Teresa N.; Smith, Kimothy L.; Schupp,
```

```
     James; Palmer, Eldon G.; Cox, Rebecca A.;    ***Keim, Paul***
CS   Department of Biological Sciences, Northern Arizona University, Flagstaff,
     AZ, 86011-5640, USA
SO   Journal of Clinical Microbiology (2003), 41(9), 4224-4230
     CODEN: JCMIDW; ISSN: 0095-1137
PB   American Society for Microbiology
DT   Journal
LA   English
AB   Mol. epidemiol. tools for genotyping clin. isolates of Mycobacterium
       ***tuberculosis***   have been developed and used to help track and
     contain transmission of   ***tuberculosis***  . We identified 87 short
     sequence repeat loci within the genome of the M.   ***tuberculosis***
     H37Rv strain. Nine tandem repeats were found to be variable (variable-no.
     tandem repeats [VNTRs]) in a set of 91 isolates. Fifty-seven of the
     isolates had only four IS6110 bands. The other 34 isolates were members
     of the Beijing strain family. The no. of alleles of each these nine VNTRs
     was detd. by examg. each isolate. Six of the loci (Mtb-v1, -v4, -v10,
     -v15, -v18, and -v20) were able to differentiate the Beijing spoligotype
     identical isolates into seven distinct genotypes. Five of the loci
     (Mtb-v3, -v5, -v6, -v10, and -v15) were informative in discriminating the
     four-band IS6110 restriction fragment length polymorphism isolates from
     each other. The Nei's diversity values of each marker ranged from 0.02 to
     0.59, with the no. of alleles ranging from two to eight across the entire
     strain set. These nine loci provide a useful, discriminatory extension of
     VNTR typing methods for application to mol. epidemiol. studies of M.
       ***tuberculosis***  .
RE.CNT  23    THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT


=> e spurgiesz robert scott/au
E1            4     SPURGIESZ R S/AU
E2            2     SPURGIESZ R SCOTT/AU
E3            1 --> SPURGIESZ ROBERT SCOTT/AU
E4            1     SPURGIESZ S/AU
E5            2     SPURGIN A/AU
E6            8     SPURGIN A J/AU
E7            2     SPURGIN ANTHONY J/AU
E8            1     SPURGIN B/AU
E9            5     SPURGIN C B/AU
E10           1     SPURGIN D/AU
E11           2     SPURGIN D A/AU
E12           1     SPURGIN D D/AU

=> s e1-e3
L3            7 ("SPURGIESZ R S"/AU OR "SPURGIESZ R SCOTT"/AU OR "SPURGIESZ
                ROBERT SCOTT"/AU)

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4            3 DUP REM L3 (4 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y


L4   ANSWER 1 OF 3  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2004:80897  CAPLUS
DN   140:140628
TI   Primers and kits for genotyping Mycobacterium tuberculosis strains by
     detecting variable-number tandem repeat loci
IN   Keim, Paul S.; Schupp, James M.;   ***Spurgiesz, Robert Scott***
PA   Arizona Board of Regents, USA
SO   PCT Int. Appl., 44 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
     ---------------   ----  --------      ---------------  --------
PI   WO 2004009837      A2   20040129      WO 2003-US22950  20030721
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W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI US 2002-397224P P 20020719

AB MLVA methods for strain discrimination among Mycobacterium tuberculosum strains are disclosed. Nine VNTR loci have been identified from genomic sequences of Mycobacterium tuberculosum strains and primer pairs suitable for amplifying the VNTR by PCR are disclosed. Polymorphisms at these loci were used to resolve genotypes into distinct groups. This sub-typing scheme is useful for the epidemiol. study of Mycobacterium tuberculosum and may be applied to the local detection of the pathol. causative agent of tuberculosum.

L4 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1

AN 2003:792964 CAPLUS

DN 140:23719

TI Molecular typing of Mycobacterium tuberculosis by using nine novel variable-number tandem repeats across the Beijing family and low-copy-number IS6110 isolates

AU ***Spurgiesz, R. Scott*** ; Quitugua, Teresa N.; Smith, Kimothy L.; Schupp, James; Palmer, Eldon G.; Cox, Rebecca A.; Keim, Paul

CS Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ, 86011-5640, USA

SO Journal of Clinical Microbiology (2003), 41(9), 4224-4230
CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology

DT Journal

LA English

AB Mol. epidemiol. tools for genotyping clin. isolates of Mycobacterium tuberculosis have been developed and used to help track and contain transmission of tuberculosis. We identified 87 short sequence repeat loci within the genome of the M. tuberculosis H37Rv strain. Nine tandem repeats were found to be variable (variable-no. tandem repeats [VNTRs]) in a set of 91 isolates. Fifty-seven of the isolates had only four IS6110 bands. The other 34 isolates were members of the Beijing strain family. The no. of alleles of each these nine VNTRs was detd. by examg. each isolate. Six of the loci (Mtb-v1, -v4, -v10, -v15, -v18, and -v20) were able to differentiate the Beijing spoligotype identical isolates into seven distinct genotypes. Five of the loci (Mtb-v3, -v5, -v6, -v10, and -v15) were informative in discriminating the four-band IS6110 restriction fragment length polymorphism isolates from each other. The Nei's diversity values of each marker ranged from 0.02 to 0.59, with the no. of alleles ranging from two to eight across the entire strain set. These nine loci provide a useful, discriminatory extension of VNTR typing methods for application to mol. epidemiol. studies of M. tuberculosis.

RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 3 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 2002:608976 BIOSIS

DN PREV200200608976

TI Correlations among IS6110, spoligotyping, MIRU and MLVA in the molecular epidemiology of Mycobacterium tuberculosis.

AU ***Spurgiesz, R. S.*** [Reprint author]; Smith, K. [Reprint author]; Keim, P. [Reprint author]; Steinlein, L.; Crawford, J.; Quitugua, T.; Robisin, R.; Abert, H.

CS Northern Arizona University, Flagstaff, AZ, USA

SO Abstracts of the General Meeting of the American Society for Microbiology, (2002) Vol. 102, pp. 477. print.
Meeting Info.: 102nd General Meeting of the American Society for Microbiology. Salt Lake City, UT, USA. May 19-23, 2002. American Society for Microbiology.
ISSN: 1060-2011.

```
DT   Conference; (Meeting)
     Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 27 Nov 2002
     Last Updated on STN: 27 Nov 2002
AB   Mycobacterium tuberculosis extracts a tremendous cost in human lives each
     year worldwide. The tuberculosis epidemiology would benefit from an
     improvements molecular typing system. Currently, IS6110 and spoligotyping
     are most widely used in the typing of M. tuberculosis. More recently,
     MIRU (mycobacterium interspersed repetitive unit) and MLVA (Multi-locus
     variable number tandem repeat analysis) have shown to be rapid and
     reproducible methods. MLVA typing was effective across 108 isolates
     collected in Utah between 1995-2000. MIRU and MLVA both use PCR to
     amplify various VNTR loci in the genome of M. tuberculosis. Genotype
     correlations amongst IS6110 and spoligotyping have been found previously.
     Similar associations between spoligotyping and MLVA have been found using
     88 closely related strains from Texas. In this study, we analyze data
     from all four typing methods across 180 isolates collected throughout the
     United States between 1995-2000. Cluster analysis was performed for each
     data type individually and, then, collectively across all methods. MIRU
     results in combination with MLVA have comparable discrimination equivalent
     to the combined results of IS6110 and spoligotyping. Thus, MIRU and MLVA
     demonstrate a reliable, rapid, and discriminatory typing system. These
     VNTR methods could be an important contribution to the field of molecular
     epidemiology of M. tuberculosis.


=> e schupp james m/au
E1            1     SCHUPP J RALPH/AU
E2            6     SCHUPP JAMES/AU
E3           19 --> SCHUPP JAMES M/AU
E4           16     SCHUPP JAMES R/AU
E5            1     SCHUPP JAN/AU
E6            4     SCHUPP JANE/AU
E7           15     SCHUPP JANE E/AU
E8            1     SCHUPP JIM/AU
E9            4     SCHUPP JOACHIM/AU
E10           4     SCHUPP JOHANNES/AU
E11           3     SCHUPP JOHN/AU
E12           7     SCHUPP JOHN D/AU

=> se2-e3 and tubercul?
SE2-E3 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s e2-e3 and tubercul?
L5            3 ("SCHUPP JAMES"/AU OR "SCHUPP JAMES M"/AU) AND TUBERCUL?

=> dup rem l5
PROCESSING COMPLETED FOR L5
L6             2 DUP REM L5 (1 DUPLICATE REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 2 ANSWERS - CONTINUE? Y/(N):y

L6   ANSWER 1 OF 2  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2004:80897  CAPLUS
DN   140:140628
TI   Primers and kits for genotyping Mycobacterium   ***tuberculosis***
     strains by detecting variable-number tandem repeat loci
IN   Keim, Paul S.;   ***Schupp, James M.***  ; Spurgiesz, Robert Scott
PA   Arizona Board of Regents, USA
SO   PCT Int. Appl., 44 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
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PI   WO 2004009837     A2   20040129       WO 2003-US22950  20030721
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM,
             PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN,
             TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG,
             KZ, MD, RU, TJ
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
             CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC,
             NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
             GW, ML, MR, NE, SN, TD, TG
PRAI US 2002-397224P   P    20020719
AB   MLVA methods for strain discrimination among Mycobacterium
       ***tuberculosum***   strains are disclosed. Nine VNTR loci have been
     identified from genomic sequences of Mycobacterium   ***tuberculosum***
     strains and primer pairs suitable for amplifying the VNTR by PCR are
     disclosed. Polymorphisms at these loci were used to resolve genotypes
     into distinct groups. This sub-typing scheme is useful for the epidemiol.
     study of Mycobacterium   ***tuberculosum***   and may be applied to the
     local detection of the pathol. causative agent of   ***tuberculosum***  .

L6   ANSWER 2 OF 2  CAPLUS  COPYRIGHT 2004 ACS on STN  DUPLICATE 1
AN   2003:792964  CAPLUS
DN   140:23719
TI   Molecular typing of Mycobacterium   ***tuberculosis***   by using nine
     novel variable-number tandem repeats across the Beijing family and
     low-copy-number IS6110 isolates
AU   Spurgiesz, R. Scott; Quitugua, Teresa N.; Smith, Kimothy L.;   ***Schupp,***
  ***     James***  ; Palmer, Eldon G.; Cox, Rebecca A.; Keim, Paul
CS   Department of Biological Sciences, Northern Arizona University, Flagstaff,
     AZ, 86011-5640, USA
SO   Journal of Clinical Microbiology (2003), 41(9), 4224-4230
     CODEN: JCMIDW; ISSN: 0095-1137
PB   American Society for Microbiology
DT   Journal
LA   English
AB   Mol. epidemiol. tools for genotyping clin. isolates of Mycobacterium
       ***tuberculosis***   have been developed and used to help track and
     contain transmission of   ***tuberculosis***  . We identified 87 short
     sequence repeat loci within the genome of the M.   ***tuberculosis***
     H37Rv strain. Nine tandem repeats were found to be variable (variable-no.
     tandem repeats [VNTRs]) in a set of 91 isolates. Fifty-seven of the
     isolates had only four IS6110 bands. The other 34 isolates were members
     of the Beijing strain family. The no. of alleles of each these nine VNTRs
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     -v15, -v18, and -v20) were able to differentiate the Beijing spoligotype
     identical isolates into seven distinct genotypes. Five of the loci
     (Mtb-v3, -v5, -v6, -v10, and -v15) were informative in discriminating the
     four-band IS6110 restriction fragment length polymorphism isolates from
     each other. The Nei's diversity values of each marker ranged from 0.02 to
     0.59, with the no. of alleles ranging from two to eight across the entire
     strain set. These nine loci provide a useful, discriminatory extension of
     VNTR typing methods for application to mol. epidemiol. studies of M.
       ***tuberculosis***  .
RE.CNT  23    THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT


=> s tubercul? and ((vntr)or(variable number tandem repeat))
L7         304 TUBERCUL? AND ((VNTR) OR(VARIABLE NUMBER TANDEM REPEAT))

=> dup rem l7
PROCESSING COMPLETED FOR L7
L8          145 DUP REM L7 (159 DUPLICATES REMOVED)

=> s l8 and ((MLVA)or(multi-locus vntr analysis))
L9           3 L8 AND ((MLVA) OR(MULTI-LOCUS VNTR ANALYSIS))

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y
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L9 ANSWER 1 OF 3 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:608976 BIOSIS
DN PREV200200608976
TI Correlations among IS6110, spoligotyping, MIRU and ***MLVA*** in the molecular epidemiology of Mycobacterium ***tuberculosis*** .
AU Spurgiesz, R. S. [Reprint author]; Smith, K. [Reprint author]; Keim, P. [Reprint author]; Steinlein, L.; Crawford, J.; Quitugua, T.; Robisin, R.; Abert, H.
CS Northern Arizona University, Flagstaff, AZ, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2002) Vol. 102, pp. 477. print.
Meeting Info.: 102nd General Meeting of the American Society for Microbiology. Salt Lake City, UT, USA. May 19-23, 2002. American Society for Microbiology.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 27 Nov 2002
Last Updated on STN: 27 Nov 2002
AB Mycobacterium ***tuberculosis*** extracts a tremendous cost in human lives each year worldwide. The ***tuberculosis*** epidemiology would benefit from an improvements molecular typing system. Currently, IS6110 and spoligotyping are most widely used in the typing of M. ***tuberculosis*** . More recently, MIRU (mycobacterium interspersed repetitive unit) and ***MLVA*** (Multi-locus ***variable*** ***number*** ***tandem*** ***repeat*** analysis) have shown to be rapid and reproducible methods. ***MLVA*** typing was effective across 108 isolates collected in Utah between 1995-2000. MIRU and ***MLVA*** both use PCR to amplify various ***VNTR*** loci in the genome of M. ***tuberculosis*** . Genotype correlations amongst IS6110 and spoligotyping have been found previously. Similar associations between spoligotyping and ***MLVA*** have been found using 88 closely related strains from Texas. In this study, we analyze data from all four typing methods across 180 isolates collected throughout the United States between 1995-2000. Cluster analysis was performed for each data type individually and, then, collectively across all methods. MIRU results in combination with ***MLVA*** have comparable discrimination equivalent to the combined results of IS6110 and spoligotyping. Thus, MIRU and ***MLVA*** demonstrate a reliable, rapid, and discriminatory typing system. These ***VNTR*** methods could be an important contribution to the field of molecular epidemiology of M. ***tuberculosis*** .

L9 ANSWER 2 OF 3 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:251637 BIOSIS
DN PREV200200251637
TI ***Multi*** - ***Locus*** ***VNTR*** ***analysis*** (***MLVA***) for identification and epidemiological tracking of Mycobacterium ***tuberculosis*** .
AU Spurgiesz, S. [Reprint author]; Albert, H.; Smith, K. [Reprint author]; Keys, C. [Reprint author]; Robison, R.; Keim, P. [Reprint author]
CS Northern Arizona University, Flagstaff, AZ, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2001) Vol. 101, pp. 702. print.
Meeting Info.: 101st General Meeting of the American Society for Microbiology. Orlando, FL, USA. May 20-24, 2001. American Society for Microbiology.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 24 Apr 2002
Last Updated on STN: 24 Apr 2002
AB Molecular typing as an aid for epidemiological investigations is an effective method for identifying and tracking infectious pathogens. This is somewhat problematic for Mycobacterium ***tuberculosis*** because of the high degree of monomorphism among strains. Commonly, typing is accomplished using spoligotyping or restriction fragment polymorphisms based upon insertion element probes. An alternative approach is to use a PCR-based method that utilizes the rapidly evolving sequences: variable

number tandemly repeats (VNTRs). Multiple Locus ***VNTR*** Analysis (***MLVA***) is capable of resolving even closely related strains. We have identified many potential ***VNTR*** loci in the M. ***tuberculosis*** genome and converted a subset into a ***MLVA*** typing system. The conversion process from potential marker loci sequences to informative markers was apprx80% successful. We have used ***MLVA*** to examine 108 clinical isolates collected in Utah; about half of which were cultured from foreign immigrants. ***MLVA*** -based genetic distances were analyzed using clustering methods to identify genetic affinities. These genetic relationships suggest possible ***tuberculosis*** transmission patterns. Future studies involving ***MLVA*** will have a greater genetic resolution and be able to handle a large number of samples.

L9 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:80897 CAPLUS
DN 140:140628
TI Primers and kits for genotyping Mycobacterium ***tuberculosis*** strains by detecting ***variable*** - ***number*** ***tandem*** ***repeat*** loci
IN Keim, Paul S.; Schupp, James M.; Spurgiesz, Robert Scott
PA Arizona Board of Regents, USA
SO PCT Int. Appl., 44 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004009837	A2	20040129	WO 2003-US22950	20030721

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI US 2002-397224P P 20020719
AB ***MLVA*** methods for strain discrimination among Mycobacterium ***tuberculosum*** strains are disclosed. Nine ***VNTR*** loci have been identified from genomic sequences of Mycobacterium ***tuberculosum*** strains and primer pairs suitable for amplifying the ***VNTR*** by PCR are disclosed. Polymorphisms at these loci were used to resolve genotypes into distinct groups. This sub-typing scheme is useful for the epidemiol. study of Mycobacterium ***tuberculosum*** and may be applied to the local detection of the pathol. causative agent of ***tuberculosum*** .

=> d l8 bib ab 1-
YOU HAVE REQUESTED DATA FROM 145 ANSWERS - CONTINUE? Y/(N):y

L8 ANSWER 1 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:80897 CAPLUS
DN 140:140628
TI Primers and kits for genotyping Mycobacterium ***tuberculosis*** strains by detecting ***variable*** - ***number*** ***tandem*** ***repeat*** loci
IN Keim, Paul S.; Schupp, James M.; Spurgiesz, Robert Scott
PA Arizona Board of Regents, USA
SO PCT Int. Appl., 44 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

PI WO 2004009837 A2 20040129 WO 2003-US22950 20030721
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2002-397224P P 20020719
AB MLVA methods for strain discrimination among Mycobacterium ***tuberculosum*** strains are disclosed. Nine ***VNTR*** loci have been identified from genomic sequences of Mycobacterium ***tuberculosum*** strains and primer pairs suitable for amplifying the ***VNTR*** by PCR are disclosed. Polymorphisms at these loci were used to resolve genotypes into distinct groups. This sub-typing scheme is useful for the epidemiol. study of Mycobacterium ***tuberculosum*** and may be applied to the local detection of the pathol. causative agent of ***tuberculosum*** .

L8 ANSWER 2 OF 145 USPATFULL on STN
AN 2004:144546 USPATFULL
TI Bacillus stearothermophilus SSB protein and use thereof
IN O'Donnell, Michael E., Hastings-on-Hudson, NY, UNITED STATES
Yuzhakov, Alexander, Malden, MA, UNITED STATES
Yurieva, Olga, New York, NY, UNITED STATES
Jeruzalmi, David, Cambridge, MA, UNITED STATES
Bruck, Irina, New York, NY, UNITED STATES
Kuriyan, John, Berkeley, CA, UNITED STATES
PI US 2004110210 A1 20040610
AI US 2003-673119 A1 20030926 (10)
RLI Continuation of Ser. No. US 2000-716964, filed on 21 Nov 2000, PENDING Continuation-in-part of Ser. No. US 2000-642218, filed on 18 Aug 2000, PENDING Continuation of Ser. No. US 1998-57416, filed on 8 Apr 1998, ABANDONED
PRAI US 1997-43202P 19970408 (60)
DT Utility
FS APPLICATION
LREP Nixon Peabody LLP, Clinton Square, P.O. Box 31051, Rochester, NY, 14603-1051
CLMN Number of Claims: 7
ECL Exemplary Claim: 1
DRWN 82 Drawing Page(s)
LN.CNT 9522
AB The present invention relates to an isolated DNA molecule from a thermophilic bacterium which encodes a DNA polymerase III-type enzyme subunit. Also encompassed by the present invention are host cells and expression system including the heterologous DNA molecule of the present invention, as well as isolated replication enzyme subunits encoded by such DNA molecules. Also disclosed is a method of producing a recombinant thermostable DNA polymerase III-type enzyme, or subunit thereof, from a thermophilic bacterium, which is carried out by transforming a host cell with at least one heterologous DNA molecule of the present invention under conditions suitable for expression of the DNA polymerase III-type enzyme, or subunit thereof, and then isolating the DNA polymerase III-type enzyme, or subunit thereof.

L8 ANSWER 3 OF 145 USPATFULL on STN
AN 2004:138964 USPATFULL
TI Nucleic acid encoding bacillus stearothermophilus SSB protein
IN O'Donnell, Michael E., Hastings-on Hudson, NY, UNITED STATES
Yuzhakov, Alexander, Malden, MA, UNITED STATES
Yurieva, Olga, New York, NY, UNITED STATES
Jeruzalmi, David, Cambridge, MA, UNITED STATES
Bruck, Irina, New York, NY, UNITED STATES
Kuriyan, John, Berkeley, CA, UNITED STATES
PI US 2004106137 A1 20040603
AI US 2003-670817 A1 20030925 (10)

RLI Continuation of Ser. No. US 2000-716964, filed on 21 Nov 2000, PENDING Continuation-in-part of Ser. No. US 2000-642218, filed on 18 Aug 2000, PENDING Continuation of Ser. No. US 1998-57416, filed on 8 Apr 1998, ABANDONED
PRAI US 1997-43202P 19970408 (60)
DT Utility
FS APPLICATION
LREP Nixon Peabody LLP, Clinton Square, P.O. Box 31051, Rochester, NY, 14603-1051
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 82 Drawing Page(s)
LN.CNT 9513
AB The present invention relates to an isolated DNA molecule from a thermophilic bacterium which encodes a DNA polymerase III-type enzyme subunit. Also encompassed by the present invention are host cells and expression system including the heterologous DNA molecule of the present invention, as well as isolated replication enzyme subunits encoded by such DNA molecules. Also disclosed is a method of producing a recombinant thermostable DNA polyrnerase III-type enzyme, or subunit thereof, from a thermophilic bacterium, which is carried out by transforming a host cell with at least one heterologous DNA molecule of the present invention under conditions suitable for expression of the DNA polymerase III-type enzyme, or subunit thereof, and then isolating the DNA polymerase III-type enzyme, or subunit thereof.

L8 ANSWER 4 OF 145 USPATFULL on STN
AN 2004:133299 USPATFULL
TI DIRECT MULTIPLEX CHARACTERIZATION OF GENOMIC DNA
IN Willis, Thomas D., San Francisco, CA, UNITED STATES
Hardenbol, Paul, Los Altos, CA, UNITED STATES
Jain, Maneesh, Menlo Park, CA, UNITED STATES
Stolc, Viktor, Cupertino, CA, UNITED STATES
Ronaghi, Mostafa, Palo Alto, CA, UNITED STATES
Davis, Ronald W., Palo Alto, CA, UNITED STATES
PI US 2004101835 A1 20040527
AI US 2001-999362 A1 20011024 (9)
PRAI US 2000-242901P 20001024 (60)
DT Utility
FS APPLICATION
LREP DORSEY & WHITNEY LLP, Suite 3400, Four Embarcadero Center, San Francisco, CA, 94111-4187
CLMN Number of Claims: 47
ECL Exemplary Claim: 1
DRWN 18 Drawing Page(s)
LN.CNT 4346
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention is directed to novel methods of multiplexing nucleic acid reactions, including amplification, detection and genotyping. The invention relies on the use of precircle probes that are circularized in the presence of the corresponding target nucleic acids, cleaved, and then amplified.

L8 ANSWER 5 OF 145 USPATFULL on STN
AN 2004:107595 USPATFULL
TI Bacillus stearothermophilus beta polymerase subunit and use thereof
IN O'Donnell, Michael E., Hastings-on-Hudson, NY, UNITED STATES
Yuzhakov, Alexander, Malden, MA, UNITED STATES
Yurieva, Olga, New York, NY, UNITED STATES
Jeruzalmi, David, New York, NY, UNITED STATES
Bruck, Irina, New York, NY, UNITED STATES
Kuriyan, John, Berkeley, CA, UNITED STATES
PI US 2004081995 A1 20040429
AI US 2003-673127 A1 20030926 (10)
RLI Continuation of Ser. No. US 2000-716964, filed on 21 Nov 2000, PENDING Continuation-in-part of Ser. No. US 2000-642218, filed on 18 Aug 2000, PENDING Continuation of Ser. No. US 1998-57416, filed on 8 Apr 1998, ABANDONED
PRAI US 1997-43202P 19970408 (60)
DT Utility
FS APPLICATION

LREP Nixon Peabody LLP, Clinton Square, P.O. Box 31051, Rochester, NY, 14603-1051
CLMN Number of Claims: 8
ECL Exemplary Claim: 1
DRWN 82 Drawing Page(s)
LN.CNT 9515
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to an isolated DNA molecule from a thermophilic bacterium which encodes a DNA polymerase III-type enzyme subunit. Also encompassed by the present invention are host cells and expression system including the heterologous DNA molecule of the present invention, as well as isolated replication enzyme subunits encoded by such DNA molecules. Also disclosed is a method of producing a recombinant thermostable DNA polymerase III-type enzyme, or subunit thereof, from a thermophilic bacterium, which is carried out by transforming a host cell with at least one heterologous DNA molecule of the present invention under conditions suitable for expression of the DNA polymerase III-type enzyme, or subunit thereof, and then isolating the DNA polymerase III-type enzyme, or subunit thereof.

L8 ANSWER 6 OF 145 USPATFULL on STN
AN 2004:101150 USPATFULL
TI Bacillus stearothermophilus polc polymerase subunit and use thereof
IN O'Donnell, Michael E., Hastings-on-Hudson, NY, UNITED STATES
Yuzhakov, Alexander, Malden, MA, UNITED STATES
Yurieva, Olga, New York, NY, UNITED STATES
Jeruzalmi, David, Cambridge, MA, UNITED STATES
Bruck, Irina, New York, NY, UNITED STATES
Kuriyan, John, Berkeley, CA, UNITED STATES
PI US 2004077012 A1 20040422
AI US 2003-672638 A1 20030926 (10)
RLI Continuation of Ser. No. US 2000-716964, filed on 21 Nov 2000, PENDING Continuation-in-part of Ser. No. US 2000-642218, filed on 18 Aug 2000, PENDING Continuation of Ser. No. US 1998-57416, filed on 8 Apr 1998, ABANDONED
PRAI US 1997-43202P 19970408 (60)
DT Utility
FS APPLICATION
LREP Nixon Peabody LLP, Clinton Square, P.O. Box 31051, Rochester, NY, 14603-1051
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 82 Drawing Page(s)
LN.CNT 9511
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to an isolated DNA molecule from a thermophilic bacterium which encodes a DNA polymerase III-type enzyme subunit. Also encompassed by the present invention are host cells and expression system including the heterologous DNA molecule of the present invention, as well as isolated replication enzyme subunits encoded by such DNA molecules. Also disclosed is a method of producing a recombinant thermostable DNA polymerase III-type enzyme, or subunit thereof, from a thermophilic bacterium, which is carried out by transforming a host cell with at least one heterologous DNA molecule of the present invention under conditions suitable for expression of the DNA polymerase III-type enzyme, or subunit thereof, and then isolating the DNA polymerase III-type enzyme, or subunit thereof.

L8 ANSWER 7 OF 145 USPATFULL on STN
AN 2004:89119 USPATFULL
TI Human single nucleotide polymorphisms in organic anion transport and multi-drug resistant proteins
IN Tsuchihashi, Zenta, Pennington, NJ, UNITED STATES
Hui, Lester, Fairfax, VA, UNITED STATES
Kirchgessner, Todd, North Wales, PA, UNITED STATES
PI US 2004068096 A1 20040408
AI US 2002-252155 A1 20020920 (10)
PRAI US 2001-324172P 20010921 (60)
US 2001-333700P 20011127 (60)
DT Utility
FS APPLICATION

LREP STEPHEN B. DAVIS, BRISTOL-MYERS SQUIBB COMPANY, PATENT DEPARTMENT, P O BOX 4000, PRINCETON, NJ, 08543-4000
CLMN Number of Claims: 19
ECL Exemplary Claim: 1
DRWN 125 Drawing Page(s)
LN.CNT 18439
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides polynucleotides and polypeptides corresponding to novel gene sequences associated with the incidence of liver disease, and resistance to statin drugs, particularly pravastatin. The invention also provides polynucleotide fragments corresponding to the genomic and/or coding regions of these genes which comprise at least one polymorphic site per fragment. Allele-specific primers and probes which hybridize to these regions, and/or which comprise at least one polymorphic site are also provided. The polynucleotides, primers, and probes of the present invention are useful in phenotype correlations, paternity testing, medicine, and genetic analysis. Also provided are vectors, host cells, antibodies, and recombinant and synthetic methods for producing said polypeptides. The invention further relates to diagnostic and therapeutic methods for applying these novel polypeptides to the diagnosis, treatment, and/or prevention of various, diseases and/or disorders, particularly hepatic and cardiovascular diseases related to these polypeptides, such as liver disease and high cholesterol. The invention further relates to screening methods for identifying agonists and antagonists of the polynucleotides and polypeptides of the present invention.

L8 ANSWER 8 OF 145 USPATFULL on STN
AN 2004:57413 USPATFULL
TI Nucleic acid encoding aquifex aeolicus delta prime polymerase subunit
IN O'Donnell, Michael E., Hastings-on-Hudson, NY, UNITED STATES
Yuzhakov, Alexander, Malden, MA, UNITED STATES
Yurieva, Olga, New York, NY, UNITED STATES
Jeruzalmi, David, Cambridge, MA, UNITED STATES
Bruck, Irina, New York, NY, UNITED STATES
Kuriyan, John, Berkeley, CA, UNITED STATES
PI US 2004043415 A1 20040304
AI US 2003-671134 A1 20030925 (10)
RLI Continuation of Ser. No. US 2000-716964, filed on 21 Nov 2000, PENDING Continuation-in-part of Ser. No. US 2000-642218, filed on 18 Aug 2000, PENDING Continuation of Ser. No. US 1998-57416, filed on 8 Apr 1998, ABANDONED
PRAI US 1997-43202P 19970408 (60)
DT Utility
FS APPLICATION
LREP Nixon Peabody LLP, Clinton Square, P.O. Box 31051, Rochester, NY, 14603-1051
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 82 Drawing Page(s)
LN.CNT 9517
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to an isolated DNA molecule from a thermophilic bacterium which encodes a DNA polymerase III-type enzyme subunit. Also encompassed by the present invention are host cells and expression system including the heterologous DNA molecule of the present invention, as well as isolated replication enzyme subunits encoded by such DNA molecules. Also disclosed is a method of producing a recombinant thermostable DNA polymerase III-type enzyme, or subunit thereof, from a thermophilic bacterium, which is carried out by transforming a host cell with at least one heterologous DNA molecule of the present invention under conditions suitable for expression of the DNA polymerase III-type enzyme, or subunit thereof, and then isolating the DNA polymerase III-type enzyme, or subunit thereof.

L8 ANSWER 9 OF 145 USPATFULL on STN
AN 2004:57412 USPATFULL
TI Nucleic acid encoding bacillus stearothermophilus tau polymerase subunit
IN O'Donnell, Michael E., Hastings-on- Hudson, NY, UNITED STATES
Yuzhakov, Alexander, Malden, MA, UNITED STATES
Yurieva, Olga, New York, NY, UNITED STATES

Jeruzalmi, David, Cambridge, MA, UNITED STATES
Bruck, Irina, New York, NY, UNITED STATES
Kuriyan, John, Berkeley, CA, UNITED STATES
PI US 2004043414 A1 20040304
AI US 2003-670844 A1 20030925 (10)
RLI Continuation of Ser. No. US 2000-716964, filed on 21 Nov 2000, PENDING Continuation-in-part of Ser. No. US 2000-642218, filed on 18 Aug 2000, PENDING Continuation of Ser. No. US 1998-57416, filed on 8 Apr 1998, ABANDONED
PRAI US 1997-43202P 19970408 (60)
DT Utility
FS APPLICATION
LREP Nixon Peabody LLP, Clinton Square, P.O. Box 31051, Rochester, NY, 14603-1051
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 82 Drawing Page(s)
LN.CNT 9513
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to an isolated DNA molecule from a thermophilic bacterium which encodes a DNA polymerase III-type enzyme subunit. Also encompassed by the present invention are host cells and expression system including the heterologous DNA molecule of the present invention, as well as isolated replication enzyme subunits encoded by such DNA molecules. Also disclosed is a method of producing a recombinant thermostable DNA polymerase III-type enzyme, or subunit thereof, from a thermophilic bacterium, which is carried out by transforming a host cell with at least one heterologous DNA molecule of the present invention under conditions suitable for expression of the DNA polymerase III-type enzyme, or subunit thereof, and then isolating the DNA polymerase III-type enzyme, or subunit thereof.

L8 ANSWER 10 OF 145 USPATFULL on STN
AN 2004:50861 USPATFULL
TI Nucleic acid encoding thermotoga maritima delta prime polymerase subunit
IN O'Donnell, Michael E., Hastings-on-Hudson, NY, UNITED STATES
Yuzhakov, Alexander, Malden, MA, UNITED STATES
Yurieva, Olga, New York, NY, UNITED STATES
Jeruzalmi, David, Cambridge, MA, UNITED STATES
Bruck, Irina, New York, NY, UNITED STATES
Kuriyan, John, Berkeley, MA, UNITED STATES
PI US 2004038290 A1 20040226
AI US 2003-671419 A1 20030925 (10)
RLI Continuation of Ser. No. US 2000-716964, filed on 21 Nov 2000, PENDING Continuation-in-part of Ser. No. US 2000-642218, filed on 18 Aug 2000, PENDING Continuation of Ser. No. US 1998-57416, filed on 8 Apr 1998, ABANDONED
PRAI US 1997-43202P 19970408 (60)
DT Utility
FS APPLICATION
LREP Nixon Peabody LLP, Clinton Square, P.O. Box 31051, Rochester, NY, 14603-1051
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 82 Drawing Page(s)
LN.CNT 9513
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to an isolated DNA molecule from a thermophilic bacterium which encodes a DNA polymerase III-type enzyme subunit. Also encompassed by the present invention are host cells and expression system including the heterologous DNA molecule of the present invention, as well as isolated replication enzyme subunits encoded by such DNA molecules. Also disclosed is a method of producing a recombinant thermostable DNA polymerase III-type enzyme, or subunit thereof, from a thermophilic bacterium, which is carried out by transforming a host cell with at least one heterologous DNA molecule of the present invention under conditions suitable for expression of the DNA polymerase III-type enzyme, or subunit thereof, and then isolating the DNA polymerase III-type enzyme, or subunit thereof.

L8 ANSWER 11 OF 145 USPATFULL on STN

AN 2004:50860 USPATFULL
TI Nucleic acid encoding bacillus stearothermophilus delta polymerase subunit
IN O'Donnell, Michael E., Hastings-on-Hudson, NY, UNITED STATES
Yuzhakov, Alexander, Malden, MA, UNITED STATES
Yurieva, Olga, New York, NY, UNITED STATES
Jeruzalmi, David, Cambridge, MA, UNITED STATES
Bruck, Irina, New York, NY, UNITED STATES
Kuriyan, John, Berkeley, CA, UNITED STATES
PI US 2004038289 A1 20040226
AI US 2003-671403 A1 20030925 (10)
RLI Continuation of Ser. No. US 2000-716964, filed on 21 Nov 2000, PENDING Continuation-in-part of Ser. No. US 2000-642218, filed on 18 Aug 2000, PENDING Continuation of Ser. No. US 1998-57416, filed on 8 Apr 1998, ABANDONED
PRAI US 1997-43202P 19970408 (60)
DT Utility
FS APPLICATION
LREP Nixon Peabody LLP, Clinton Square, P.O. Box 31051, Rochester, NY, 14603-1051
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 82 Drawing Page(s)
LN.CNT 9518
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to an isolated DNA molecule from a thermophilic bacterium which encodes a DNA polymerase III-type enzyme subunit. Also encompassed by the present invention are host cells and expression system including the heterologous DNA molecule of the present invention, as well as isolated replication enzyme subunits encoded by such DNA molecules. Also disclosed is a method of producing a recombinant thermostable DNA polymerase III-type enzyme, or subunit thereof, from a thermophilic bacterium, which is carried out by transforming a host cell with at least one heterologous DNA molecule of the present invention under conditions suitable for expression of the DNA polymerase III-type enzyme, or subunit thereof, and then isolating the DNA polymerase III-type enzyme, or subunit thereof.

L8 ANSWER 12 OF 145 USPATFULL on STN
AN 2004:44589 USPATFULL
TI Human single nucleotide polymorphisms
IN Edmonds, Manling-Ma, Lawrenceville, PA, UNITED STATES
Hui, Lester, Fairfax, VA, UNITED STATES
Perrone, Mark, Boston, MA, UNITED STATES
Powell, James R., Lumberville, PA, UNITED STATES
Ramanathan, Chandra S., Wallingford, CT, UNITED STATES
Swanson, Brian, Yardley, PA, UNITED STATES
Tsuchihashi, Zenta, Skillman, NJ, UNITED STATES
Zerba, Kim, New Hope, PA, UNITED STATES
PI US 2004033582 A1 20040219
AI US 2003-453827 A1 20030603 (10)
PRAI US 2002-384980P 20020603 (60)
DT Utility
FS APPLICATION
LREP STEPHEN B. DAVIS, BRISTOL-MYERS SQUIBB COMPANY, PATENT DEPARTMENT, P O BOX 4000, PRINCETON, NJ, 08543-4000
CLMN Number of Claims: 19
ECL Exemplary Claim: 1
DRWN 32 Drawing Page(s)
LN.CNT 20032
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides polynucleotides and polypeptides corresponding to novel gene sequences associated with the incidence of cardiovascular disorders. The invention also provides polynucleotide fragments corresponding to the genomic and/or coding regions of these genes which comprise at least one polymorphic site per fragment. Allele-specific primers and probes which hybridize to these regions, and/or which comprise at least one polymorphic site are also provided. The polynucleotides, primers, and probes of the present invention are useful in phenotype correlations, paternity testing, medicine, and genetic analysis. Also provided are vectors, host cells, antibodies, and

recombinant and synthetic methods for producing said polypeptides. The invention further relates to diagnostic and therapeutic methods for applying these novel polypeptides to the diagnosis, treatment, and/or prevention of various diseases and/or disorders, particularly cardiovascular diseases related to these polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of the polynucleotides and polypeptides of the present invention.

L8 ANSWER 13 OF 145 USPATFULL on STN
AN 2004:18781 USPATFULL
TI Detection of heteroduplex polynucleotides using mutant nucleic acid repair enzymes with attenuated catalytic activity
IN Yuan, Chong-Sheng, San Diego, CA, UNITED STATES
Datta, Abhijit, Carlsbad, CA, UNITED STATES
PI US 2004014083 A1 20040122
AI US 2003-373238 A1 20030224 (10)
RLI Continuation-in-part of Ser. No. US 2000-514016, filed on 25 Feb 2000, PENDING
DT Utility
FS APPLICATION
LREP Peng Chen, Morrison & Foerster LLP, Suite 500, 3811 Valley Centre Drive, San Diego, CA, 92130-2332
CLMN Number of Claims: 105
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 10442
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods for detecting, localizing and removing abnormal base-pairing in a nucleic acid duplex are provided. These methods can be used for prognosis and diagnosis of diseases, disorders, pathogenic infections and nucleic acid polymorphisms. Combinations, kits and articles of manufacture for use in these methods are also provided.

L8 ANSWER 14 OF 145 USPATFULL on STN
AN 2004:135719 USPATFULL
TI Therapeutic methods relating to human carbamyl phosphate synthetase I polymorphism
IN Summar, Marshall L., Brentwood, TN, United States
Christman, Brian W., Nashville, TN, United States
PA Vanderbilt University, Nashville, TN, United States (U.S. corporation)
PI US 6743823 B1 20040601
AI US 2000-585077 20000601 (9)
RLI Continuation-in-part of Ser. No. US 1999-323472, filed on 1 Jun 1999, now patented, Pat. No. US 6346382
DT Utility
FS GRANTED
EXNAM Primary Examiner: Myers, Carla J.; Assistant Examiner: Johannsen, Diana
LREP Jenkins, Wilson & Taylor, P.A.
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN 0 Drawing Figure(s); 12 Drawing Page(s)
LN.CNT 5559
AB Isolated polynucleotide molecules and peptides encoded by these molecules are used in the analysis of human carbamyl phosphate synthetase I phenotypes, as well as in diagnostic and therapeutic applications, relating to a human carbamyl phosphate synthetase I polymorphism. By analyzing genomic DNA or amplified genomic DNA, or amplified cDNA derived from mRNA, it is possible to type a human carbamyl phosphate synthetase I with regard to the human carbamyl phosphate synthetase I polymorphism, for example, in the context of diagnosing and treating hepatic veno-occlusive disease (HVOD) associated with bone marrow transplants.

L8 ANSWER 15 OF 145 USPATFULL on STN
AN 2004:4504 USPATFULL
TI Tumor necrosis factor receptor 2
IN Stanton, Jr., Vincent P., Belmont, MA, United States
PA Nuvelo, Inc., Sunnyvale, CA, United States (U.S. corporation)
PI US 6673908 B1 20040106
AI US 2001-968455 20011001 (9)

RLI Division of Ser. No. US 2000-649035, filed on 25 Aug 2000 Continuation-in-part of Ser. No. US 2000-590749, filed on 8 Jun 2000, now abandoned Continuation-in-part of Ser. No. US 2000-495780, filed on 1 Feb 2000, now abandoned Continuation-in-part of Ser. No. US 2000-492712, filed on 27 Jan 2000, now abandoned Continuation-in-part of Ser. No. WO 2000-US1392, filed on 20 Jan 2000 Continuation-in-part of Ser. No. US 968455 Continuation-in-part of Ser. No. US 1999-451252, filed on 29 Nov 1999, now abandoned Continuation-in-part of Ser. No. US 1999-427835, filed on 26 Oct 1999, now abandoned Continuation-in-part of Ser. No. US 1999-414330, filed on 6 Oct 1999, now abandoned Continuation-in-part of Ser. No. US 1999-389993, filed on 3 Sep 1999, now abandoned Continuation-in-part of Ser. No. US 1999-370841, filed on 9 Aug 1999, now abandoned Continuation-in-part of Ser. No. US 1999-300747, filed on 26 Apr 1999, now abandoned
PRAI US 1999-131334P 19990426 (60)
US 1999-131191P 19990426 (60)
US 1999-121047P 19990222 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Benzion, Gary; Assistant Examiner: Chakrabarti, Arun Kr.
LREP Fish & Richardson P.C.
CLMN Number of Claims: 10
ECL Exemplary Claim: 1
DRWN 0 Drawing Figure(s); 0 Drawing Page(s)
LN.CNT 17463
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present disclosure describes the use of genetic variance information for genes involved in inflammatory or immunologic disease, disorder, or dysfunction. The variance information is indicative of the expected response of a patient to a method of treatment. Methods of determining relevant variance information and additional methods of using such variance information are also described.

L8 ANSWER 16 OF 145 MEDLINE on STN
AN 2004248330 IN-PROCESS
DN PubMed ID: 15131159
TI Use of mycobacterial interspersed repetitive unit- ***variable*** - ***number*** ***tandem*** ***repeat*** typing to examine genetic diversity of Mycobacterium ***tuberculosis*** in Singapore.
AU Sun Yong-Jiang; Bellamy Richard; Lee Ann S G; Ng Sze Ta; Ravindran Sindhu; Wong Sin-Yew; Locht Camille; Supply Philip; Paton Nicholas I
CS Department of Infectious Diseases, Tan Tock Seng Hospital, Singapore, Republic of Singapore.. Yong_Jiang_Sun@ttsh.com.sg
NC N01 AI-75320 (NIAID)
SO Journal of clinical microbiology, (2004 May) 42 (5) 1986-93. Journal code: 7505564. ISSN: 0095-1137.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20040519
Last Updated on STN: 20040520
AB Strain typing using variable-number tandem repeats of mycobacterial interspersed repetitive units (MIRU- ***VNTR***) is a powerful tool for studying the epidemiology and genetic relationships of Mycobacterium ***tuberculosis*** isolates. For this study, isolates from 291 patients in Singapore were genotyped by this method. One hundred sixty-six distinct MIRU- ***VNTR*** patterns were detected. One hundred sixty-two strains were grouped into 1 of 35 different MIRU- ***VNTR*** clusters and 131 isolates were unique. In this sample collection, 9 of the 12 MIRU- ***VNTR*** loci were moderately or highly discriminative according to their allelic diversities. The Hunter-Gaston discriminatory index was 0.975, indicating the high power of discrimination of MIRU- ***VNTR*** typing. By direct comparisons with previously typed MIRU- ***VNTR*** patterns and by genetic relationship analyses, we could identify and clearly define four epidemic groups of M. ***tuberculosis*** in our sample, corresponding to the W/Beijing, East-Africa-Indian, Haarlem, and Delhi genotype families. Furthermore, MIRU- ***VNTR*** typing was able to clearly distinguish ancestral and modern M. ***tuberculosis*** strains as defined by TbD1 genomic

deletion analysis. These results indicate that MIRU- ***VNTR*** typing can be a useful first-line tool for studying the genetic diversity of M. ***tuberculosis*** isolates in a large urban setting such as Singapore.

L8 ANSWER 17 OF 145 MEDLINE on STN
AN 2004248328 IN-PROCESS
DN PubMed ID: 15131145
TI Use of genome level-informed PCR as a new investigational approach for analysis of outbreak-associated Mycobacterium ***tuberculosis*** isolates.
AU Rajakumar Kumar; Shafi Jamila; Smith Rebecca J; Stabler Richard A; Andrew Peter W; Modha Deborah; Bryant Gerry; Monk Philip; Hinds Jason; Butcher Philip D; Barer Michael R
CS Department of Infection, Immunity and Inflammation, Leicester Medical School, University of Leicester, and Department of Clinical Microbiology, University Hospitals of Leicester NHS Trust, Leicester LE1 5WW, United Kingdom.
SO Journal of clinical microbiology, (2004 May) 42 (5) 1890-6.
Journal code: 7505564. ISSN: 0095-1137.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20040519
Last Updated on STN: 20040520
AB Mycobacterium ***tuberculosis*** strain CH, the index isolate linked to a major ***tuberculosis*** outbreak associated with high levels of transmissibility and virulence, was characterized by microarray analysis by use of a PCR product array representative of the genome of M. ***tuberculosis*** strain H37Rv. Seven potential genomic deletions were identified in CH, five of which were confirmed by PCR analysis across the predicted deletion points. The panel of five PCRs required to individually interrogate these loci was collectively referred to as the genome level-informed PCR (GLIP) assay. GLIP analysis was performed with CH, 12 other epidemiologically linked isolates, and 43 recent, non-outbreak-associated isolates derived from patients within the local area. All 13 outbreak-linked isolates showed a profile corresponding to the presence of all five deletions. These 13 isolates were also found to share common ***variable*** - ***number*** ***tandem*** ***repeat*** and mycobacterial interspersed repetitive unit profiles. None of the 43 non-outbreak-associated isolates exhibited the five-deletion profile. Although three individual deletions were present in upwards of 44% of the non-outbreak-associated isolates, no single-deletion isolates were detected. Interestingly, none of these deletions had been previously recognized, and sequence analysis of the immediate flanking regions in CH failed to identify a likely mechanism of deletion for four of the five loci. The GLIP assay also proved valuable in ongoing surveillance of the outbreak, rapidly identifying a further two outbreak-associated cases months after the initial cluster and, importantly, dismissing a further 12 epidemiologically suspect cases, which allowed the optimum deployment of public health resources.

L8 ANSWER 18 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
AN 2004:220761 CAPLUS
TI Genotypic analysis of Mycobacterium ***tuberculosis*** in Bangladesh and prevalence of the Beijing strain
AU Banu, Sayera; Gordon, Stephen V.; Palmer, Si; Islam, Reazul; Ahmed, Shakeel; Alam, Khan Mashrequl; Cole, Stewart T.; Brosch, Roland
CS ICDDR,B: Centre for Health and Population Research, Dhaka, 1000, Bangladesh
SO Journal of Clinical Microbiology (2004), 42(2), 674-682
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Genotypic anal. was performed on 48 Mycobacterium ***tuberculosis*** complex strains collected from a hospital in Dhaka city. Deletion anal. showed that the isolates were all M. ***tuberculosis*** ; 13 of them were found to be of the "ancestral" type, while 35 were of the "modern" type, indicating that both endemic (ancestral type) and epidemic (modern type) strains cause ***tuberculosis*** in Bangladesh. Genotyping

based on the spoligotype and variable-no. tandem repeats (***VNTR***) of mycobacterial interspersed repetitive units (MIRU) was also done. A total of 34 strains (71%) were grouped by spoligotyping into nine different clusters; the largest comprised 15 isolates of the Beijing genotype, whereas the remaining eight clusters consisted of two to five isolates. MIRU- ***VNTR*** typing detected 32 different patterns among 44 tested strains, and the 15 Beijing strains were further discriminated by MIRU- ***VNTR*** typing (7 distinct patterns for the 15 isolates). These results indicate that MIRU- ***VNTR*** typing, along with spoligotyping and deletion anal., can be used effectively for mol. epidemiol. studies to det. ongoing transmission clusters; to our knowledge, this is the first report about the type of strains prevailing in Bangladesh.

RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 19 OF 145 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN DUPLICATE 2
AN 2004029368 EMBASE
TI Molecular Epidemiology of Disease Due to Mycobacterium bovis in Humans in the United Kingdom.
AU Gibson A.L.; Hewinson G.; Goodchild T.; Watt B.; Story A.; Inwald J.; Drobniewski F.A.
CS A.L. Gibson, Mycobacterium Reference Unit, Health Protection Agency, Dulwich Hospital, East Dulwich Grove, London SE22 8QF, United Kingdom. andreagibson78@hotmail.com
SO Journal of Clinical Microbiology, (2004) 42/1 (431-434).
Refs: 19
ISSN: 0095-1137 CODEN: JCMIDW
CY United States
DT Journal; Article
FS 004 Microbiology
017 Public Health, Social Medicine and Epidemiology
LA English
SL English
AB Mycobacterium bovis is the causative agent of bovine ***tuberculosis*** , with a wide host range. Fifty human M. bovis isolates were typed using spoligotyping and variable number tandem repeats (***VNTR***). Fifteen of these spoligotypes have not yet been recorded in cattle. The predominant spoligotype in humans and cattle was subdivided by ***VNTR*** .

L8 ANSWER 20 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3
AN 2004:328813 CAPLUS
TI LVNTR-typing of Mycobacterium ***tuberculosis*** cultures from the Samara region by the variable number of tandem repeats
AU Zheltkova, E.; Raddi, M.; Malomanova, N.; Elizarova, E.; Melentyev, A.; Mutovkin, E.; Zakharova, S.; Fedorin, I.; Chernousova, L.; Drobinevsky, F.
CS Central Research Institute of Tuberculosis, Mowcow, Russia
SO Zhurnal Mikrobiologii, Epidemiologii i Immunobiologii (2004), (1), 35-37
CODEN: ZMEIAV; ISSN: 0372-9311
PB S-info
DT Journal
LA Russian
AB To type Mycobacterium ***tuberculosis*** (MT) strains by the variable no. of tandem repeats (***VNTR***), 136 MT cultures, isolated in 5 main general therapeutic labs. and penitentiary antituberculosis institutions of the Samara region, were studied: Gene typing revealed that the greatest no. of MT strains (73) belonged to ***VNTR*** type 42435. It was followed by ***VNTR*** type 42435. It was followed by ***VNTR*** type 22232, found in 13 isolated cultures. Among the MT cultures of the most widely spread ***VNTR*** type 42435, rifampicin-resistant strains prevailed (57 strains, i.e. 78%), while strains belonging to ***VNTR*** type 22232 were mainly sensitive to rifampicin (84%). ***VNTR*** typing of MT typing may be useful for epidemiol. studies in the field of phthisiol.

L8 ANSWER 21 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:402339 CAPLUS
TI Molecular genetic typing of mycobacteria
AU Nikolaevskii, V. V.; Bazhora, Yu. I.

CS Odess. Gos. Med. Univ., Odessa, Ukraine
SO Dosyagnennya Biologii ta Meditsini (2004), (1), 28-34
CODEN: DBMOA8
PB Odes'kii Derzhavnii Medichnii Universitet
DT Journal
LA Russian
AB This is review of recent publications on the problems of genotyping of Mycobacterium ***tuberculosis*** and its application in diagnosis and mol. epidemiol. of ***tuberculosis*** . Recent methods of Mycobacteria typing, including IS6110 RFLP (Restriction Fragments Length Polymorphism), ***VNTR*** (Variable No. Tandem Repeats), spoligotyping and their modifications are described. A particular attention is paid to advantages, shortcomings and modes of practical application of the certain methods. Practical usefulness of mol. epidemiol. studies is demonstrated. Urgent issues regarding implementation of mol. typing technique in clin. microbiol. practice in Ukraine, creation of national data-bases and their integration in international programs are proposed.

L8 ANSWER 22 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 4
AN 2004:112260 BIOSIS
DN PREV200400112814
TI Molecular differentiation of Mycobacterium bovis isolates. Review of main techniques and applications.
AU Haddad, Nadia [Reprint Author]; Masselot, Monique; Durand, B.
CS Ecole Nationale Veterinaire, U.P. Maladies Contagieuses, Maisons-Alfort, France
nhaddad@vet-alfort.fr
SO Research in Veterinary Science, (February 2004) Vol. 76, No. 1, pp. 1-18. print.
CODEN: RVTSA9. ISSN: 0034-5288.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 25 Feb 2004
Last Updated on STN: 25 Feb 2004
AB Until recently, none of the Mycobacterium bovis typing techniques permitted a satisfactory differentiation of isolates. During the last 10 years, the genome of pathogenic mycobacteria has been extensively studied, and phylogenetic analyses have shown that all (except Mycobacterium avium) belong to a single genetic species: the Mycobacterium ***tuberculosis*** complex. This increase in knowledge about the genome of these bacteria has lead to the discovery of molecular markers that allow us to differentiate isolates. Because of the phylogenetic proximity of the strains, even if most of these markers have been discovered in M. ***tuberculosis*** , they could be successfully adapted to the other bacteria of the M. ***tuberculosis*** complex, especially M. bovis. The most common markers in use today are the IS6110 insertion sequence, the direct repeat (DR) region, the poly(GC) rich (PGRS) sequences and the variable number tandem repeats (***VNTR***) sequences. The corresponding typing techniques are briefly described, and current knowledge of polymorphism and marker stability is detailed. If molecular markers are to offer wide perspectives for field studies, these two characteristics (polymorphism and stability) must be taken into account when choosing the marker(s) used in a study. In this context, examples of the application of molecular typing techniques for M. bovis are reviewed, on the one hand with epidemiological studies for which the major problem is the comparison between isolates and, on the other, with more general studies about the population genetics of M. bovis in a given country, and about its history and its phylogeny.

L8 ANSWER 23 OF 145 USPATFULL on STN
AN 2003:335014 USPATFULL
TI Functional polymorphisms of the interleukin-1 locus affecting transcription and susceptibility to inflammatory and infectious diseases
IN Wyllie, David, Oxford, UNITED KINGDOM
Duff, Gordon, Sheffield, UNITED KINGDOM
Aziz, Nazneen, Lexington, MA, UNITED STATES
Hsieh, Chung-Ming, West Roxbury, MA, UNITED STATES
Kornman, Kenneth, Newton, MA, UNITED STATES
PI US 2003235890 A1 20031225

AI US 2002-300011 A1 20021119 (10)
PRAI US 2002-386020P 20020605 (60)
US 2001-331681P 20011119 (60)
DT Utility
FS APPLICATION
LREP Ivor R. Elrifi, Mintz, Levin, Cohn, Ferris,, Glovsky and Popeo, P.C., One Financial Center, Boston, MA, 02111
CLMN Number of Claims: 23
ECL Exemplary Claim: 1
DRWN 23 Drawing Page(s)
LN.CNT 3423
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides methods and reagents for detecting a polymorphism associated with in an upstream region of the interleukin-1 beta (IL-B) gene (IL-1B (-3737)) that affects transcription of the gene and susceptibility to inflammatory and infectious diseases such as periodontal disease and Alzheimer's disease.

L8 ANSWER 24 OF 145 USPATFULL on STN
AN 2003:330152 USPATFULL
TI Fatty acid transport proteins
IN Stahl, Andreas, Allston, MA, UNITED STATES
Hirsch, David J., Jamaica Plain, MA, UNITED STATES
Lodish, Harvey F., Brookline, MA, UNITED STATES
Gimeno, Ruth E., Wellesley, MA, UNITED STATES
Tartaglia, Louis A., Newton, MA, UNITED STATES
PI US 2003232363 A1 20031218
AI US 2003-405877 A1 20030401 (10)
RLI Division of Ser. No. US 2000-611197, filed on 6 Jul 2000, ABANDONED Continuation-in-part of Ser. No. US 2000-506252, filed on 17 Feb 2000, ABANDONED Continuation-in-part of Ser. No. US 1999-465280, filed on 16 Dec 1999, ABANDONED Continuation-in-part of Ser. No. US 1999-405504, filed on 23 Sep 1999, PENDING Continuation-in-part of Ser. No. US 1999-405505, filed on 23 Sep 1999, ABANDONED Continuation-in-part of Ser. No. US 1999-232197, filed on 14 Jan 1999, GRANTED, Pat. No. US 6300096 Continuation-in-part of Ser. No. US 1999-232200, filed on 14 Jan 1999, GRANTED, Pat. No. US 6288213 Continuation-in-part of Ser. No. US 1999-232201, filed on 14 Jan 1999, GRANTED, Pat. No. US 6348321 Continuation-in-part of Ser. No. US 1999-232195, filed on 14 Jan 1999, PENDING Continuation-in-part of Ser. No. US 1999-232191, filed on 14 Jan 1999, GRANTED, Pat. No. US 6284487
PRAI US 1998-110941P 19981204 (60)
US 1998-93491P 19980720 (60)
US 1998-71374P 19980115 (60)
DT Utility
FS APPLICATION
LREP HAMILTON, BROOK, SMITH & REYNOLDS, P.C., 530 VIRGINIA ROAD, P.O. BOX 9133, CONCORD, MA, 01742-9133
CLMN Number of Claims: 97
ECL Exemplary Claim: 1
DRWN 148 Drawing Page(s)
LN.CNT 11047
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A family of fatty acid transport proteins (FATPs) mediate transport of long chain fatty acids (LCFAs) across cell membranes into cells. These proteins exhibit different expression patterns among the organs of mammals. Nucleic acids encoding FATPs of this family, vectors comprising these nucleic acids, as well as the production of FATP proteins in host cells are described. Also described are methods to test FATPs for fatty acid transport function, and methods to identify inhibitors or enhancers of transport function. The altering of LCFA uptake by administering to the mammal an inhibitor or enhancer of FATP transport function of a FATP in the small intestine can decrease or increase calories available as fats, and can decrease or increase circulating fatty acids. The organ specificity of FATP distribution can be exploited in methods to direct drugs, diagnostic indicators and so forth to an organ such as the heart.

L8 ANSWER 25 OF 145 USPATFULL on STN
AN 2003:330113 USPATFULL
TI Chimeric alphavirus replicon particles
IN Polo, John M., Hayward, CA, UNITED STATES

Perri, Silvia, Castro Valley, CA, UNITED STATES
Thudium, Kent, Oakland, CA, UNITED STATES
Tang, Zequn, San Ramon, CA, UNITED STATES
PA Chiron Corporation (U.S. corporation)
PI US 2003232324 A1 20031218
AI US 2002-310734 A1 20021204 (10)
RLI Continuation-in-part of Ser. No. US 2002-123101, filed on 11 Apr 2002, PENDING
PRAI US 2001-295451P 20010531 (60)
DT Utility
FS APPLICATION
LREP Chiron Corporation, Intellectual Property, P.O. Box 8097, Emeryville, CA, 94662-8097
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN 15 Drawing Page(s)
LN.CNT 3743
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Chimeric alphaviruses and alphavirus replicon particles are provided including methods of making and using same. Specifically, alphavirus particles are provided having nucleic acid molecules derived from one or more alphaviruses and structural proteins (capsid and/or envelope) from at least two or more alphaviruses. Methods of making, using, and therapeutic preparations containing the chimeric alphavirus particle, are disclosed.

L8 ANSWER 26 OF 145 USPATFULL on STN
AN 2003:324619 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, Lugano-Cassarate, SWITZERLAND
PI US 2003228594 A1 20031211
AI US 2003-375714 A1 20030224 (10)
RLI Continuation of Ser. No. US 2001-879341, filed on 11 Jun 2001, GRANTED, Pat. No. US 6589485 Continuation of Ser. No. US 2001-796416, filed on 28 Feb 2001, GRANTED, Pat. No. US 6500621 Continuation of Ser. No. US 2000-495444, filed on 31 Jan 2000, GRANTED, Pat. No. US 6300076 Continuation of Ser. No. US 2000-504245, filed on 15 Feb 2000, GRANTED, Pat. No. US 6221605 Continuation of Ser. No. US 1999-287679, filed on 6 Apr 1999, GRANTED, Pat. No. US 6258538 Continuation of Ser. No. US 1996-617256, filed on 18 Mar 1996, GRANTED, Pat. No. US 6043031 Continuation-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995, GRANTED, Pat. No. US 5605798
DT Utility
FS APPLICATION
LREP Stephanie Seidman, Heller Ehrman White & McAuliffe LLP, 7th Floor, 4350 La Jolla Village Drive, San Diego, CA, 92122-1246
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN 57 Drawing Page(s)
LN.CNT 2643
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting particular nucleic acid molecules and mutations in the molecules are provided.

L8 ANSWER 27 OF 145 USPATFULL on STN
AN 2003:318669 USPATFULL
TI Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
IN Shimkets, Richard A., West Haven, CT, UNITED STATES
Leach, Martin, Webster, MA, UNITED STATES
PI US 2003224413 A1 20031204
AI US 2003-393815 A1 20030320 (10)
RLI Continuation of Ser. No. US 1999-442129, filed on 16 Nov 1999, ABANDONED
PRAI US 1998-109024P 19981117 (60)
DT Utility
FS APPLICATION
LREP MINTZ, LEVIN, COHN, FERRIS,, GLOVSKY AND POPEO, P.C., One Financial Center, Boston, MA, 02111
CLMN Number of Claims: 44
ECL Exemplary Claim: 1

DRWN No Drawings
LN.CNT 6779
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides nucleic acids containing single-nucleotide polymorphisms identified for transcribed human sequences, as well as methods of using the nucleic acids.

L8 ANSWER 28 OF 145 USPATFULL on STN
AN 2003:312177 USPATFULL
TI Novel human neurotransmitter transporter
IN Sharma, Rahul, Gurnee, IL, UNITED STATES
Ramanathan, Chandra S., Wallingford, CT, UNITED STATES
Westphal, Ryan, Chesire, CT, UNITED STATES
Feder, John N., Belle Mead, NJ, UNITED STATES
Lee, Liana M., North Brunswick, NJ, UNITED STATES
PI US 2003219774 A1 20031127
AI US 2002-319315 A1 20021213 (10)
PRAI US 2001-340436P 20011214 (60)
DT Utility
FS APPLICATION
LREP STEPHEN B. DAVIS, BRISTOL-MYERS SQUIBB COMPANY, PATENT DEPARTMENT, P O BOX 4000, PRINCETON, NJ, 08543-4000
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 15 Drawing Page(s)
LN.CNT 8684
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides a novel human orphan neurotransmitter transporter belonging to the family of Na.sup.+/Cl.sup.- dependent transporters. Inventive HNTTBMY1 polypeptides and polynucleotides and methods for producing such polypeptides by recombinant techniques are disclosed. Further provided are methods for utilizing these polypeptides and polynucleotides in therapy and diagnostic assays for such. The transporter of the present invention is expressed highly in the amygdala brain subregion, which is known to be associated with affective disorders. The inventive transporter shares high homology with the rat orphan neurotransmitter transporter termed NTT4.

L8 ANSWER 29 OF 145 USPATFULL on STN
AN 2003:244300 USPATFULL
TI Method of examining foreign matter derived from living body
IN Shirasaki, Yoshinari, Tsukuba-shi, JAPAN
Nishimura, Naoyuki, Tsukuba-shi, JAPAN
PI US 2003170709 A1 20030911
AI US 2003-370759 A1 20030224 (10)
PRAI JP 2002-60923 20020306
DT Utility
FS APPLICATION
LREP David T. Nikaido, RADER, FISHMAN & GRAUER PLLC, Suite 501, 1233 20th Street, N.W., Washington, DC, 20036
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 662
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a method for examining a foreign matter derived from a living body in quality control for production of various products in order to rapidly identify an individual from whom a living body-derived material contaminated as a foreign matter in products or facilities involved in production of the products was derived, while securing the secret of information on nucleic acid sequences unique to individuals. The method for examining a foreign matter derived from a living body includes identifying an individual from whom a living body-derived material contaminated as a foreign matter in products or facilities involved in production of the products was derived, on the basis of information on sequences of nucleic acid contained in the living body-derived material.

L8 ANSWER 30 OF 145 USPATFULL on STN
AN 2003:237708 USPATFULL
TI Methods of analysis of nucleic acids

IN Hinkel, Christopher A., San Diego, CA, UNITED STATES
Kimmerly, William J., Agoura Hills, CA, UNITED STATES
Yang, Li, San Diego, CA, UNITED STATES
PI US 2003165865 A1 20030904
AI US 2002-56908 A1 20020125 (10)
PRAI US 2001-264972P 20010129 (60)
US 2001-266186P 20010202 (60)
US 2001-295986P 20010604 (60)
DT Utility
FS APPLICATION
LREP TORREY MESA RESEARCH INSTITUTE, INTELLECTUAL PROPERTY DEPARTMENT, 3115 MERRYFIELD ROW, SAN DIEGO, CA, 92121
CLMN Number of Claims: 35
ECL Exemplary Claim: 1
DRWN 1 Drawing Page(s)
LN.CNT 2291
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods are provided for the multiplex analysis of polynucleotide expression and single nucleotide polymorphism detection using capture probes coupled to uniquely identified particles. The methods provided are characterized by high flexibility and high throughput.

L8 ANSWER 31 OF 145 USPATFULL on STN
AN 2003:213625 USPATFULL
TI Chimeric alphavirus replicon particles
IN Polo, John M., Hayward, CA, UNITED STATES
Perri, Silvia, Castro Valley, CA, UNITED STATES
Thudium, Kent, Oakland, CA, UNITED STATES
PI US 2003148262 A1 20030807
AI US 2002-123101 A1 20020411 (10)
PRAI US 2001-295451P 20010531 (60)
DT Utility
FS APPLICATION
LREP CHIRON CORPORATION, Intellectual Property - R440, P.O. Box 8097, Emeryville, CA, 94662-8097
CLMN Number of Claims: 48
ECL Exemplary Claim: 1
DRWN 13 Drawing Page(s)
LN.CNT 3668
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Chimeric alphaviruses and alphavirus replicon particles are provided including methods of making and using same. Specifically, alphavirus particles are provided having nucleic acid molecules derived from one or more alphaviruses and structural proteins (capsid and/or envelope) from at least two or more alphaviruses. Methods of making, using, and therapeutic preparations containing the chimeric alphavirus particle, are disclosed.

L8 ANSWER 32 OF 145 USPATFULL on STN
AN 2003:196058 USPATFULL
TI NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH THE SUCROSE PATHWAY
IN CHEIKH, NORDINE, MANCHESTER, MO, UNITED STATES
FISHER, DANE K, O'FALLON, MO, UNITED STATES
LIU, JINGDONG, BALLWIN, MO, UNITED STATES
PI US 2003135870 A1 20030717
AI US 1999-237183 A1 19990126 (9)
RLI Continuation-in-part of Ser. No. US 1998-210297, filed on 8 Dec 1998, ABANDONED Continuation-in-part of Ser. No. US 1998-199129, filed on 24 Nov 1998, PENDING Continuation-in-part of Ser. No. US 1999-229413, filed on 12 Jan 1999, ABANDONED
PRAI US 1997-67000P 19971124 (60)
US 1997-69472P 19971209 (60)
US 1998-72888P 19980127 (60)
US 1998-74201P 19980210 (60)
US 1998-74282P 19980210 (60)
US 1998-74280P 19980210 (60)
US 1998-74281P 19980210 (60)
US 1998-74566P 19980212 (60)
US 1998-74567P 19980212 (60)
US 1998-74565P 19980212 (60)

PI US 1998-75462P 19980219 (60)
US 1998-74789P 19980219 (60)
US 1998-75459P 19980219 (60)
US 1998-75461P 19980219 (60)
US 1998-75464P 19980219 (60)
US 1998-75460P 19980219 (60)
US 1998-75463P 19980219 (60)
US 1998-76912P 19980306 (60)
US 1998-77231P 19980309 (60)
US 1998-77229P 19980309 (60)
US 1998-77230P 19980309 (60)
US 1998-78368P 19980318 (60)
US 1998-80844P 19980407 (60)
US 1998-83067P 19980427 (60)
US 1998-83386P 19980429 (60)
US 1998-83387P 19980429 (60)
US 1998-83388P 19980429 (60)
US 1998-83389P 19980429 (60)
US 1998-83390P 19980429 (60)
US 1998-85224P 19980513 (60)
US 1998-85223P 19980513 (60)
US 1998-85222P 19980513 (60)
US 1998-86186P 19980521 (60)
US 1998-86187P 19980521 (60)
US 1998-86185P 19980521 (60)
US 1998-86184P 19980521 (60)
US 1998-86183P 19980521 (60)
US 1998-86188P 19980521 (60)
US 1998-87422P 19980601 (60)
US 1998-89524P 19980616 (60)
US 1998-89810P 19980618 (60)
US 1998-89814P 19980618 (60)
US 1998-89793P 19980618 (60)
US 1998-90170P 19980622 (60)
US 1998-90928P 19980626 (60)
US 1998-91035P 19980629 (60)
US 1998-91405P 19980630 (60)
US 1998-92036P 19980708 (60)
US 1998-99667P 19980909 (60)
US 1998-99670P 19980909 (60)
US 1998-99697P 19980909 (60)
US 1998-100674P 19980916 (60)
US 1998-100673P 19980916 (60)
US 1998-100672P 19980916 (60)
US 1998-101131P 19980921 (60)
US 1998-101132P 19980921 (60)
US 1998-101130P 19980921 (60)
US 1998-101508P 19980922 (60)
US 1998-101344P 19980922 (60)
US 1998-101347P 19980922 (60)
US 1998-101343P 19980922 (60)
US 1998-101707P 19980925 (60)
US 1998-104126P 19981013 (60)
US 1998-104128P 19981013 (60)
US 1998-104127P 19981013 (60)
US 1998-104124P 19981013 (60)
US 1998-104123P 19981013 (60)
US 1998-109018P 19981119 (60)
US 1998-108996P 19981118 (60)
US 1998-111981P 19981211 (60)
US 1998-113224P 19981222 (60)
DT Utility
FS APPLICATION
LREP ARNOLD & PORTER, IP DOCKETING DEPARTMENT, RM 1126(b), 555 12TH STREET, N.W., WASHINGTON, DC, 20004-1206
CLMN Number of Claims: 6
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 12372
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention is in the field of plant biochemistry. More

specifically the invention relates to nucleic acid sequences from plant cells, in particular, nucleic acid sequences from maize and soybean plants associated with the sucrose pathway. The invention encompasses nucleic acid molecules that encode proteins and fragments of proteins. In addition, the invention also encompasses proteins and fragments of proteins so encoded and antibodies capable of binding these proteins or fragments. The invention also relates to methods of using the nucleic acid molecules, proteins and fragments of proteins and antibodies, for example for genome mapping, gene identification and analysis, plant breeding, preparation of constructs for use in plant gene expression and transgenic plants.

L8 ANSWER 33 OF 145 USPATFULL on STN
AN 2003:187819 USPATFULL
TI Genetic markers for improved disease resistance in animals (NRAMP)
IN Tuggle, Christopher K., Ames, IA, UNITED STATES
Marklund, Lena, Ames, IA, UNITED STATES
Stabel, Thomas J., Ames, IA, UNITED STATES
Mellencamp, Martha A., St. Joseph, MO, UNITED STATES
Stumbaugh, Amber, San Carlos, CA, UNITED STATES
PI US 2003129609 A1 20030710
AI US 2002-160948 A1 20020531 (10)
PRAI US 2001-294757P 20010531 (60)
DT Utility
FS APPLICATION
LREP MCKEE, VOORHEES & SEASE, P.L.C., 801 GRAND AVENUE, SUITE 3200, DES MOINES, IA, 50309-2721
CLMN Number of Claims: 57
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 2115
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method for determining improved innate immunity, disease resistance or performance in animals is disclosed. The method involves assays for a genetic differences in the NRAMP1 gene of the animal which is associated with superior disease resistance. Novel NRAMP1 sequence, assays, and compositions for identifying the presence of absence of these alleles are provided.

L8 ANSWER 34 OF 145 USPATFULL on STN
AN 2003:187799 USPATFULL
TI DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
IN KOSTER, HUBERT, LA JOLLA, CA, UNITED STATES
LOUGH, DAVID M., BERWICKSHIRE, UNITED KINGDOM
XIANG, GOUBING, SAN DIEGO, CA, UNITED STATES
PI US 2003129589 A1 20030710
AI US 1999-297576 A1 19990628 (9)
WO 1997-US20444 19971106
DT Utility
FS APPLICATION
LREP STEPHANIE L SEIDMAN, HELLER EHRMAN WHITE & MCAULIFFE, 4350 LA JOLLA VILLAGE DRIVE, 6TH FLOOR, SAN DIEGO, CA, 92037
CLMN Number of Claims: 103
ECL Exemplary Claim: 1
DRWN 123 Drawing Page(s)
LN.CNT 10079
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting a particular nucleic acid sequence in a biological sample are provided. Depending on the sequence to be detected, the processes can be used, for example, to diagnose a genetic disease or chromosomal abnormality; a predisposition to a disease or condition, infection by a pathogenic organism, or for determining identity or heredity.

L8 ANSWER 35 OF 145 USPATFULL on STN
AN 2003:165871 USPATFULL
TI Human single nucleotide polymorphisms
IN Tsuchihashi, Zenta, Pennington, NJ, UNITED STATES
Hui, Lester, Fairfax, VA, UNITED STATES
Zerba, Kim, New Hope, PA, UNITED STATES
Ma-Edmonds, Manling, Lawrenceville, NJ, UNITED STATES

Perrone, Mark, Princeton, NJ, UNITED STATES
Swanson, Brian, Yardley, PA, UNITED STATES
Powell, James, Lumberville, PA, UNITED STATES
PI US 2003113726 A1 20030619
AI US 2001-5956 A1 20011203 (10)
PRAI US 2000-251015P 20001204 (60)
US 2001-263678P 20010123 (60)
US 2001-273037P 20010302 (60)
DT Utility
FS APPLICATION
LREP STEPHEN B. DAVIS, BRISTOL-MYERS SQUIBB COMPANY, PATENT DEPARTMENT, P O BOX 4000, PRINCETON, NJ, 08543-4000
CLMN Number of Claims: 50
ECL Exemplary Claim: 1
DRWN 108 Drawing Page(s)
LN.CNT 21863
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides polynucleotides and polypeptides corresponding to novel gene sequences associated with the incidence of cardiovascular disorders. The invention also provides polynucleotide fragments corresponding to the genomic and/or coding regions of these genes which comprise at least one polymorphic site per fragment. Allele-specific primers and probes which hybridize to these regions, and/or which comprise at least one polymorphic site are also provided. The polynucleotides, primers, and probes of the present invention are useful in phenotype correlations, paternity testing, medicine, and genetic analysis. Also provided are vectors, host cells, antibodies, and recombinant and synthetic methods for producing said polypeptides. The invention further relates to diagnostic and therapeutic methods for applying these novel polypeptides to the diagnosis, treatment, and/or prevention of various diseases and/or disorders, particularly cardiovascular diseases related to these polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of the polynucleotides and polypeptides of the present invention.

L8 ANSWER 36 OF 145 USPATFULL on STN
AN 2003:93795 USPATFULL
TI Novel human genes and gene expression products I
IN Williams, Lewis T., Mill Valley, CA, UNITED STATES
Escobedo, Jaime, Alamo, CA, UNITED STATES
Innis, Michael A., Moraga, CA, UNITED STATES
Garcia, Pablo Dominguez, San Francisco, CA, UNITED STATES
Sudduth-Klinger, Julie, Kensington, CA, UNITED STATES
Reinhard, Christoph, Alameda, CA, UNITED STATES
Giese, Klause, San Francisco, CA, UNITED STATES
Randazzo, Filippo, Emeryville, CA, UNITED STATES
Kennedy, Giulia C., San Francisco, CA, UNITED STATES
Pot, David, San Francisco, CA, UNITED STATES
Kassam, Atlaf, Oakland, CA, UNITED STATES
Lamson, George, Moraga, CA, UNITED STATES
Drmanac, Radoje, Palo Alto, CA, UNITED STATES
Crkvenjakov, Radomir, Sunnyvale, CA, UNITED STATES
Dickson, Mark, Hollister, CA, UNITED STATES
Drmanac, Snezana, Palo Alto, CA, UNITED STATES
Labat, Ivan, Sunnyvale, CA, UNITED STATES
Leshkowitz, Dena, Sunnyvale, CA, UNITED STATES
Kita, David, Foster City, CA, UNITED STATES
Garcia, Veronica, Sunnyvale, CA, UNITED STATES
Jones, Lee William, Sunnyvale, CA, UNITED STATES
Stache-Crain, Birgit, Sunnyvale, CA, UNITED STATES
PI US 2003065156 A1 20030403
AI US 2002-76555 A1 20020215 (10)
RLI Continuation of Ser. No. US 1998-217471, filed on 21 Dec 1998, PENDING
PRAI US 1997-68755P 19971223 (60)
US 1998-80664P 19980403 (60)
US 1998-105234P 19981021 (60)
DT Utility
FS APPLICATION
LREP BOZICEVIC, FIELD & FRANCIS LLP, 200 MIDDLEFIELD RD, SUITE 200, MENLO PARK, CA, 94025

CLMN Number of Claims: 22
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 15408
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostic and therapeutic agents employing such novel human polymucleotides, their corresponding genes or gene products, e.g., these genes and proteins, including probes, antisense constructs, and antibodies.

L8 ANSWER 37 OF 145 USPATFULL on STN
AN 2003:64662 USPATFULL
TI Human genes and gene expression products
IN Williams, Lewis T., Mill Valley, CA, UNITED STATES
Escobedo, Jaime, Alamo, CA, UNITED STATES
Innis, Michael A., UNITED STATES
Garcia, Pablo Dominguez, San Francisco, CA, UNITED STATES
Sudduth-Klinger, Julie, Kensington, CA, UNITED STATES
Reinhard, Christoph, Alameda, CA, UNITED STATES
Randazzo, Filippo, Oakland, CA, UNITED STATES
Kennedy, Giulia C., San Francisco, CA, UNITED STATES
Pot, David, Arlington, VA, UNITED STATES
Kassam, Altaf, Oakland, CA, UNITED STATES
Lamson, George, Moraga, CA, UNITED STATES
Drmanac, Radjoe, Palo Alto, CA, UNITED STATES
Dickson, Mark, Hollister, CA, UNITED STATES
Labat, Ivan, Mountain View, CA, UNITED STATES
Jones, Lee William, Sunnyvale, CA, UNITED STATES
Stache-Crain, Birgit, Sunnyvale, CA, UNITED STATES
PI US 2003044783 A1 20030306
AI US 2001-803719 A1 20010309 (9)
PRAI US 2000-188609P 20000309 (60)
DT Utility
FS APPLICATION
LREP Chiron Corporation Intellectual Property -R440, PO Box 8097, Emeryville, CA, 94662-8097
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 23459
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostic and therapeutic agents employing such novel human polynucleotides, their corresponding genes or gene products, e.g., these genes and proteins, including probes, antisense constructs, and antibodies.

L8 ANSWER 38 OF 145 USPATFULL on STN
AN 2003:38336 USPATFULL
TI Purified and isolated potassium-chloride cotransporter nucleic acids and polypeptides and therapeutic and screening methods using same
IN Mount, David B., Brentwood, TN, UNITED STATES
Delpire, Eric, Nashville, TN, UNITED STATES
Gamba, Gerardo, Mexico City, MEXICO
George, Alfred L., JR., Brentwood, TN, UNITED STATES
PI US 2003027983 A1 20030206
AI US 2001-835976 A1 20010416 (9)
PRAI US 2000-197350P 20000414 (60)
DT Utility
FS APPLICATION
LREP JENKINS & WILSON, PA, 3100 TOWER BLVD, SUITE 1400, DURHAM, NC, 27707
CLMN Number of Claims: 99
ECL Exemplary Claim: 1
DRWN 42 Drawing Page(s)
LN.CNT 5736
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB KCC2, KCC3 and KCC4 potassium-chloride cotransporter proteins, and nucleic acid molecules encoding the same. Recombinant host cells, recombinant nucleic acids and recombinant proteins are also disclosed, along with methods of producing each. Isolated and purified antibodies to KCC2, KCC3 and KCC4 homologs, and methods of producing the same, are also disclosed. KCC2, KCC3 and KCC4 gene products have biological activity in potassium-chloride cotransport. Thus, therapeutic methods involving this activity are also disclosed.

L8 ANSWER 39 OF 145 USPATFULL on STN
AN 2003:3430 USPATFULL
TI Mass spectrometric detection of polypeptides
IN Little, Daniel, Boston, MA, UNITED STATES
Koster, Hubert, La Jolla, CA, UNITED STATES
Higgins, G. Scott, Paisley, UNITED KINGDOM
Lough, David, Berwickshire, UNITED KINGDOM
PI US 2003003465 A1 20030102
AI US 2001-7557 A1 20011106 (10)
RLI Continuation of Ser. No. US 2000-664977, filed on 18 Sep 2000, GRANTED, Pat. No. US 6387628 Division of Ser. No. US 1998-146054, filed on 2 Sep 1998, GRANTED, Pat. No. US 6322970 Continuation-in-part of Ser. No. US 1997-922201, filed on 2 Sep 1997, GRANTED, Pat. No. US 6207370
DT Utility
FS APPLICATION
LREP HELLER EHRMAN WHITE & MCAULIFFE LLP, 4250 EXECUTIVE SQ, 7TH FLOOR, LA JOLLA, CA, 92037
CLMN Number of Claims: 19
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 4195
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A process for ascertain sequence information about a nucleic acid molecule by determining the identity of a polypeptide using mass spectroscopy is provided. Depending on the polypeptide to be identified, a process as disclosed is used, for example, to diagnose a genetic disease or chromosomal abnormality, a predisposition to a disease or condition, or infection by a pathogenic organism; or for determining identity or heredity. Kits for performing the disclosed processes also are provided.

L8 ANSWER 40 OF 145 USPATFULL on STN
AN 2003:337327 USPATFULL
TI Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
IN Shimkets, Richard A., West Haven, CT, United States
Leach, Martin, Webster, MA, United States
PA Curagen Corporation, New Haven, CT, United States (U.S. corporation)
PI US 6670464 B1 20031230
AI US 1999-443199 19991116 (9)
PRAI US 1998-109024P 19981117 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Kim, Young
LREP Elrifi, Ivor R., Kozakiewicz, Cynthia A., Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C.
CLMN Number of Claims: 28
ECL Exemplary Claim: 1
DRWN 0 Drawing Figure(s); 0 Drawing Page(s)
LN.CNT 3722
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides nucleic acids containing single-nucleotide polymorphisms identified for transcribed human sequences, as well as methods of using the nucleic acids.

L8 ANSWER 41 OF 145 USPATFULL on STN
AN 2003:314685 USPATFULL
TI Fatty acid transport proteins
IN Stahl, Andreas, Allston, MA, United States
PA Whitehead Institute for Biomedical Research, Cambridge, MA, United States (U.S. corporation)
PI US 6657049 B1 20031202

AI US 1999-232195 19990114 (9)
PRAI US 1998-110941P 19981204 (60)
US 1998-93491P 19980720 (60)
US 1998-71374P 19980115 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Nolan, Patrick J.; Assistant Examiner: Ewoldt, Gerald R.
LREP Hamilton, Brook, Smith & Reynolds, P.C.
CLMN Number of Claims: 36
ECL Exemplary Claim: 1
DRWN 202 Drawing Figure(s); 170 Drawing Page(s)
LN.CNT 9060
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Isolated antibodies and antigen-binding fragments thereof which specifically bind to members of a family of fatty acid transport proteins (FATPs) which mediate transport of long chain fatty acids (LCFAs) across cell membranes into cells are described. These proteins exhibit different expression patterns among the organs of mammals. The altering of LCFA uptake by administering to the mammal an inhibitor or enhancer of FATP transport function of a FATP in the small intestine can decrease or increase calories available as fats, and can decrease or increase circulating fatty acids. The organ specificity of FATP distribution can be exploited in methods to direct drugs, diagnostic indicators and so forth to an organ such as the heart.

L8 ANSWER 42 OF 145 USPATFULL on STN
AN 2003:209936 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, La Jolla, CA, United States
Little, Daniel P., Boston, MA, United States
Braun, Andreas, San Diego, CA, United States
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6602662 B1 20030805
AI US 2000-724877 20001128 (9)
RLI Continuation of Ser. No. US 1999-287679, filed on 6 Apr 1999, now patented, Pat. No. US 6258538 Continuation of Ser. No. US 1996-617256, filed on 18 Mar 1996, now patented, Pat. No. US 6043031 Continuation-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995, now patented, Pat. No. US 5605798
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Seidman, Stephanie L., Heller Ehrman White & McAuliffe, L.L.P.
CLMN Number of Claims: 7
ECL Exemplary Claim: 1
DRWN 87 Drawing Figure(s); 57 Drawing Page(s)
LN.CNT 2980
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting particular nucleic acid molecules and sequences in the molecules are provided. Depending upon the sequence to be detected, the processes, for example, can be used to diagnose a genetic disease or a chromosomal abnormality, a predisposition to a disease or condition, or infection by a pathogen, or for determining identity or heredity. One aspect provides a process for determining whether a target nucleotide is present in a nucleic acid molecule including hybridizing a nucleic acid molecule with a primer oligonucleotide; contacting the hybridized primer with deoxyribonucleoside triphosphates, chain terminating nucleotides and a DNA polymerase, whereby the hybridized primer is extended until a chain terminating nucleotide is incorporated, producing an extended primer, and determining the molecular mass of the extended primer, thereby determining whether the target nucleotide is present in a nucleic acid molecule.

L8 ANSWER 43 OF 145 USPATFULL on STN
AN 2003:123211 USPATFULL
TI Infrared matrix-assisted laser desorption/ionization mass spectrometric analysis of macromolecules
IN Hillenkamp, Franz, Munster, GERMANY, FEDERAL REPUBLIC OF
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)

PI US 6558902 B1 20030506
AI US 1999-307006 19990507 (9)
RLI Continuation-in-part of Ser. No. US 1998-74936, filed on 7 May 1998
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Seidman, Stephanie L., Heller Ehrman White & McAuliffe, LLP
CLMN Number of Claims: 226
ECL Exemplary Claim: 1
DRWN 3 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 8275
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Mixtures containing a biological macromolecule, such as a nucleic acid molecule or a polypeptide, and a liquid matrix, which absorbs infrared (IR) radiation, are provided. These mixtures are useful for analysis of the biological macromolecule by IR matrix assisted laser desorption/ionization (IR-MALDI) mass spectrometry. Also provided are processes for analyzing a biological macromolecule using IR-MALDI mass spectrometry. For example, processes for detecting the presence or identity of a biological macromolecule in a sample, or for sequencing a biological macromolecule are provided.

L8 ANSWER 44 OF 145 USPATFULL on STN
AN 2003:102451 USPATFULL
TI Antigen carbohydrate compounds and their use in immunotherapy
IN McKenzie, Ian F. C., Victoria, AUSTRALIA
Apostolopoulos, Vasso, Victoria, AUSTRALIA
Pietersz, Geoff Allan, Victoria, AUSTRALIA
PA Austin Research Institute, AUSTRALIA (non-U.S. corporation)
PI US 6548643 B1 20030415
AI US 2000-593870 20000614 (9)
RLI Continuation-in-part of Ser. No. US 1998-223043, filed on 30 Dec 1998, now patented, Pat. No. US 6177256 Continuation of Ser. No. US 1997-833807, filed on 9 Apr 1997, now patented, Pat. No. US 5989552 Continuation of Ser. No. US 1994-340711, filed on 16 Nov 1994, now abandoned
DT Utility
FS GRANTED
EXNAM Primary Examiner: Park, Hankyel T.
LREP Dann Dorfman Herrell and Skillman, P.C.
CLMN Number of Claims: 22
ECL Exemplary Claim: 1
DRWN 33 Drawing Figure(s); 15 Drawing Page(s)
LN.CNT 2613
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Conjugates between whole antigen or one or more repeated subunits of an antigen and a carbohydrate polymer are described. Also described are immunogenic vaccines against disease states which contain the conjugates and methods for inducing cell-mediated immune responses. The conjugates may especially contain polymers of the carbohydrate mannose and one or more repeated subunits of human mucin or non-repeated regions of human mucin.

L8 ANSWER 45 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5
AN 2003:792964 CAPLUS
DN 140:23719
TI Molecular typing of Mycobacterium ***tuberculosis*** by using nine novel variable-number tandem repeats across the Beijing family and low-copy-number IS6110 isolates
AU Spurgiesz, R. Scott; Quitugua, Teresa N.; Smith, Kimothy L.; Schupp, James; Palmer, Eldon G.; Cox, Rebecca A.; Keim, Paul
CS Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ, 86011-5640, USA
SO Journal of Clinical Microbiology (2003), 41(9), 4224-4230
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Mol. epidemiol. tools for genotyping clin. isolates of Mycobacterium ***tuberculosis*** have been developed and used to help track and contain transmission of ***tuberculosis*** . We identified 87 short

sequence repeat loci within the genome of the M. ***tuberculosis*** H37Rv strain. Nine tandem repeats were found to be variable (variable-no. tandem repeats [VNTRs]) in a set of 91 isolates. Fifty-seven of the isolates had only four IS6110 bands. The other 34 isolates were members of the Beijing strain family. The no. of alleles of each these nine VNTRs was detd. by examg. each isolate. Six of the loci (Mtb-v1, -v4, -v10, -v15, -v18, and -v20) were able to differentiate the Beijing spoligotype identical isolates into seven distinct genotypes. Five of the loci (Mtb-v3, -v5, -v6, -v10, and -v15) were informative in discriminating the four-band IS6110 restriction fragment length polymorphism isolates from each other. The Nei's diversity values of each marker ranged from 0.02 to 0.59, with the no. of alleles ranging from two to eight across the entire strain set. These nine loci provide a useful, discriminatory extension of ***VNTR*** typing methods for application to mol. epidemiol. studies of M. ***tuberculosis*** .

RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 46 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:720775 CAPLUS
DN 139:359600
TI Genomic analysis of Mycobacterium ***tuberculosis*** complex strains used for production of purified protein derivative
AU Inwald, Jacqueline; Hinds, Jason; Palmer, Si; Dale, James; Butcher, Philip D.; Hewinson, R. Glyn; Gordon, Stephen V.
CS TB Research Group, Veterinary Laboratories Agency (Weybridge), Addlestone, Surrey, KT15 3NB, UK
SO Journal of Clinical Microbiology (2003), 41(8), 3929-3932
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB The genomes of the ***tuberculin*** prodn. strains Mycobacterium bovis AN5 and Mycobacterium ***tuberculosis*** DT were compared to genome-sequenced tubercle bacilli by using DNA microarrays. Neither the AN5 nor DT strain suffered extensive gene deletions during in vitro passage. This suggests that bovine ***tuberculin*** made from M. bovis AN5 is suitable to detect infection with presently prevalent M. bovis strains.

RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 47 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 6
AN 2003:720660 CAPLUS
DN 139:359392
TI Mycobacterial interspersed repetitive unit typing of Mycobacterium ***tuberculosis*** compared to IS6110-based restriction fragment length polymorphism analysis for investigation of apparently clustered cases of ***tuberculosis***
AU Hawkey, Peter M.; Smith, E. Grace; Evans, Jason T.; Monk, Philip; Bryan, Gerry; Mohamed, Huda H.; Bardhan, Madhu; Pugh, R. Nicholas
CS Public Health Laboratory, Heartlands Hospital, Birmingham, B9 5SS, UK
SO Journal of Clinical Microbiology (2003), 41(8), 3514-3520
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB An evaluation of the utility of IS6110-based restriction fragment length polymorphism (RFLP) typing compared to a combination of variable no. tandem repeat (***VNTR***) typing and mycobacterial interspersed repetitive unit (MIRU) typing was undertaken. A total of 53 patient isolates of Mycobacterium ***tuberculosis*** from four presumed episodes of cross-infection were examd. Genomic DNA was extd. from the isolates by a cetyl trimethylammonium bromide method. The no. of copies of tandem repeats of the five loci ETRA to ETRE and 12 MIRU loci was detd. by PCR amplification and agarose gel electrophoresis of the amplicons. ***VNTR*** typing identified the major clusters of strains in the three investigations in which they occurred (each representing a different evolutionary clade: 32333, 42235, and 32433). The majority of unrelated isolates (by epidemiol. and RFLP typing) were also identified by ***VNTR*** typing. The concordance between the RFLP and MIRU typing was

complete, with the exception of two isolates with RFLP patterns that differed by one band each from the rest of the major epidemiol. linked groups of isolates in investigation A. All of these isolates had identical MIRU and ***VNTR*** types. A further pair of isolates differed in the no. of tandem repeat copies at two MIRU alleles but had identical RFLP patterns. The speed of the combined ***VNTR*** and MIRU typing approach enabled results for some of the investigations to be supplied in "real time," influencing choices in contact tracing. The ease of comparison of results of MIRU and ***VNTR*** typing, which are recorded as single multidigit nos., was also found to greatly facilitate investigation management and the communication of results to health care professionals.

RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 48 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 7
AN 2003:542680 CAPLUS
DN 140:211440
TI Evaluation of the epidemiologic utility of secondary typing methods for differentiation of Mycobacterium ***tuberculosis*** isolates
AU Kwara, Awewura; Schiro, Ronald; Cowan, Lauren S.; Hyslop, Newton E.; Wiser, Mark F.; Harrison, Stephanie Roahen; Kissinger, Patricia; Diem, Lois; Crawford, Jack T.
CS Tulane University School of Public Health and Tropical Medicine, Section of Adult Infectious Diseases, Tulane University Health Sciences Center, New Orleans, LA, 70112, USA
SO Journal of Clinical Microbiology (2003), 41(6), 2683-2685
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Spoligotyping and mycobacterial interspersed repetitive unit-variable-no. tandem repeat anal. (MIRU- ***VNTR***) were evaluated for the ability to differentiate 64 Mycobacterium ***tuberculosis*** isolates from 10 IS6110-defined clusters. MIRU- ***VNTR*** performed slightly better than spoligotyping in reducing the no. of clustered isolates and the sizes of the clusters. All epidemiol. related isolates remained clustered by MIRU- ***VNTR*** but not by spoligotyping.

RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 49 OF 145 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 2003:336347 SCISEARCH
GA The Genuine Article (R) Number: 666LZ
TI DNA fingerprinting of Salmonella enterica subsp enterica serovar Typhimurium with emphasis on phage type DT104 based on variable number of tandem repeat loci
AU Lindstedt B A (Reprint); Heir E; Gjernes E; Kapperud G
CS Norwegian Inst Publ Hlth, Div Infect Dis Control, Geitmyrsveien 75, POB 4404, N-0403 Oslo, Norway (Reprint); Norwegian Inst Publ Hlth, Div Infect Dis Control, N-0403 Oslo, Norway; Norwegian Sch Vet Sci, Dept Pharmacol Microbiol & Food Hyg, N-0033 Oslo, Norway
CYA Norway
SO JOURNAL OF CLINICAL MICROBIOLOGY, (APR 2003) Vol. 41, No. 4, pp. 1469-1479.
Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.
ISSN: 0095-1137.
DT Article; Journal
LA English
REC Reference Count: 49
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Seventy-eight human and environmental strains of Salmonella enterica subsp. enterica serovar Typhimurium, as well as 18 isolates of other Salmonella serovars and 6 isolates of Escherichia coli, were subjected to a novel variable number of tandem repeats (***VNTR***)-based fingerprinting method that showed high discrimination and reproducibility for typing serovar Typhimurium isolates. The method is based on capillary separation of PCR products from fluorescence-labeled ***VNTR*** in the serovar Typhimurium genome. The serovar Typhimurium isolates displayed 54 ***VNTR*** patterns, and the ***VNTR*** assay correctly identified

strains from a well-characterized outbreak. Among 37 serovar Typhimurium phage type DT104 isolates, 28 distinct ***VNTR*** patterns were found. This ***VNTR*** -based method is fast and suitable for complete automation. Our ***VNTR*** -based method was capable of high discrimination within the homogeneous serovar Typhimurium DT104 phage type and can be used to trace outbreaks and to monitor DT104 as well as other phage types. The ***VNTR*** assay was compared to XbaI pulsed-field gel electrophoresis, amplified fragment length polymorphism analysis, integron-cassette profiles and gene PCR of intl1, qacEDelta1, sulI1, and floR. The ***VNTR*** assay showed greatly improved resolution compared to all other tested methods in this study.

L8 ANSWER 50 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 8
AN 2003:576347 BIOSIS
DN PREV200300581548
TI Identifying Mycobacterium species and strain typing using a microfluidic labchip instrument.
AU Cooksey, Robert C. [Reprint Author]; Limor, Josef; Morlock, Glenn P.; Crawford, Jack T.
CS Tuberculosis/Mycobacteriology Branch, Centers for Disease Control and Prevention, Mail stop F-08, Atlanta, GA, 30333, USA
rcc1@cdc.gov
SO BioTechniques, (October 2003) Vol. 35, No. 4, pp. 786-794. print.
ISSN: 0736-6205 (ISSN print).
DT Article
LA English
ED Entered STN: 10 Dec 2003
Last Updated on STN: 10 Dec 2003
AB We developed schemes for rapid identification of Mycobacterium species and strain typing using a microfluidic labchip instrument. A 439-bp region of the gene that codes for the 65-kDa heat shock protein (hsp65), which has sequence polymorphisms specific for most mycobacterial species, was examined using PCR-restriction analysis (PRA). We performed PRA in duplicate, using 2 strains each of 12 species, and observed that fragment sizes (bp) determined automatically by the instrument were consistently smaller than the correct sizes for each of the species as determined by sequence analysis (mean variance, <7 bp). Mycobacterium ***tuberculosis*** isolates were typed with the labchip instrument using mycobacterial interspersed repetitive unit- ***variable*** ***number*** ***tandem*** ***repeat*** (MIRU- ***VNTR***) typing, which determines the number of copies of repeated units at 12 loci in the genome based on product size after PCR amplification. Seven strains with one to six repeat copies at each locus were examined. Sizes were smaller by a mean of 13.47 bp compared with correct sizes predicted by sequence analysis, but could be used to correctly identify all strain types. Isolates of Mycobacterium chelonae and Mycobacterium abscessus were typed using randomly amplified polymorphic DNA (RAPD) electrophoresis, and patterns obtained using the labchip instrument were compared with multilocus enzyme electrophoresis (MEE) types. Patterns were distinct and reproducible for all strains except those with closely related MEE types. The labchip instrument is a versatile alternative for sizing mycobacterial DNA fragments.

L8 ANSWER 51 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 9
AN 2003:264558 BIOSIS
DN PREV200300264558
TI Molecular methods for Mycobacterium ***tuberculosis*** strain typing: A users guide.
AU Kanduma, E.; McHugh, T. D.; Gillespie, S. H. [Reprint Author]
CS Department of Medical Microbiology, University College London, Rowland Hill Street, Royal Free Campus, London, NW3 2PF, UK
stepheng@rfc.ucl.ac.uk
SO Journal of Applied Microbiology, (2003) Vol. 94, No. 5, pp. 781-791. print.
ISSN: 1364-5072.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 4 Jun 2003

Last Updated on STN: 4 Jun 2003

AB There are now a wide range of techniques available to type Mycobacterium ***tuberculosis*** , the problem is to chose the correct technique. For large scale epidemiological studies the portability and standardization of IS6110 restriction fragment length polymorphism (RFLP) means that this remains the gold standard technique. In the next few years the internationally standard mycobacterial interspersed repetitive unit (MIRU) may come to challenge this primacy. Low copy number stains remain a problem and these can by typed by either polymorphic Guanine cytosine-rich repetitive sequence (PGRS) or MIRU-variable numbers of tandem repeat (***VNTR***). To confirm whether strains are part of a true cluster PGRS remains the method of choice. For local outbreaks and investigations of laboratory cross contamination where speed is of greatest importance suspect strains should be initially investigated using a PCR-based method. The superior reproducibility and discrimination of MIRU- ***VNTR*** means that these methods should be favoured. If matches are found, then further confirmation of identity can be achieved using IS6110 RFLP or PGRS if the strains prove to have a low IS6110 copy number.

L8 ANSWER 52 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:175162 CAPLUS
DN 139:33149
TI Molecular characterization and drug resistance patterns of strains of Mycobacterium ***tuberculosis*** isolated from patients in an AIDS counseling center in Port-au-Prince, Haiti: A 1-year study
AU Ferdinand, Severine; Sola, Christophe; Verdol, Beatrice; Legrand, Eric; Goh, Khye Seng; Berchel, Mylene; Aubery, Alexandra; Timothee, Maryse; Joseph, Patrice; Pape, Jean William; Rastogi, Nalin
CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur de Guadeloupe, Pointe-a-Pitre, F97165, Fr.
SO Journal of Clinical Microbiology (2003), 41(2), 694-702
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB ***Tuberculosis*** (TB) is one of the most common opportunistic diseases that appear among human immunodeficiency virus (HIV)-pos. patients in Haiti. In this context, the probable emergence of multidrug-resistant (MDR) strains of Mycobacterium ***tuberculosis*** is of great epidemiol. concern. However, as routine culture of M. ***tuberculosis*** and drug susceptibility testing are not performed in Haiti, it has not been possible so far to evaluate the rate of drug resistance among M. ***tuberculosis*** isolates from circulating TB cases. This report describes the first study on the mol. typing and drug resistance of M. ***tuberculosis*** isolates from patients with culture-pos. pulmonary ***tuberculosis*** monitored at the GHESKIO Centers in Haiti during the year 2000. Clin., epidemiol., and drug susceptibility testing results were available for 157 patients with confirmed cases of TB, with a total of 8.9% of patients harboring MDR M. ***tuberculosis*** . A significant assocn. between the occurrence of resistance and previous TB treatment was obsd. ($P < 0.001$), suggesting that a previous history of TB treatment was a risk factor assocd. with MDR TB in Haiti. The DNAs of individual isolates from 106 samples were available and were typed by spoligotyping and detn. of the variable no. of tandem DNA repeats. Both typing methods provided interpretable results for 96 isolates, and the clusters obsd. were further confirmed by ligation-mediated PCR to define potential cases of active transmission. Thirty-three (34%) of the isolates were found to be grouped into 11 clusters with two or more identical patterns. However, an assessment of risk factors (sex, HIV positivity, previous treatment, drug resistance) showed that none was significantly assocd. with the active transmission of TB. These observations suggest that acquired MDR TB is prevalent in Haiti and may be assocd. with compliance issues during TB treatment since prior TB therapy is the strongest risk factor assocd. with MDR TB. Prevention of TB transmission in Haiti should target active case investigation, routine detection of drug resistance, and adequate treatment of patients. The use of directly obsd. short-course therapy should be enforced throughout the country; and relapses, reactivations, or newly acquired infections should be discriminated by genotyping methods.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 53 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 10
AN 2003:88336 BIOSIS
DN PREV200300088336
TI Linkage disequilibrium between minisatellite loci supports clonal evolution of Mycobacterium ***tuberculosis*** in a high ***tuberculosis*** incidence area.
AU Supply, Philip [Reprint Author]; Warren, Robin M.; Banuls, Anne-Laure; Lesjean, Sarah; van der Spuy, Gian D.; Lewis, Lee-Anne; Tibayrenc, Michel; Van Helden, Paul D.; Locht, Camille
CS Laboratoire des Mecanismes Moleculaires de la Pathogenese Bacterienne, INSERM U447, Institut Pasteur de Lille, 1, Rue du Prof. Calmette, F-59019, Lille Cedex, France
philip.supply@pasteur-lille.fr
SO Molecular Microbiology, (January 2003) Vol. 47, No. 2, pp. 529-538. print.
ISSN: 0950-382X (ISSN print).
DT Article
LA English
ED Entered STN: 12 Feb 2003
Last Updated on STN: 12 Feb 2003
AB Deciphering the structure of pathogen populations is instrumental for the understanding of the epidemiology and history of infectious diseases and for their control. Although Mycobacterium ***tuberculosis*** is the most widespread infectious agent in humans, its actual population structure has remained hypothetical until now because: (i) its structural genes are poorly polymorphic; (ii) adequate samples and appropriate statistics for population genetic analysis have not been considered. To investigate this structure, we analysed the statistical associations (linkage disequilibrium) between 12 independent M. ***tuberculosis*** minisatellite-like loci by high-throughput genotyping within a model population of 209 isolates representative of the genetic diversity in an area with a very high incidence of ***tuberculosis*** . These loci contain variable number tandem repeats (VNTRs) of genetic elements named mycobacterial interspersed repetitive units (MIRUs). Highly significant linkage disequilibrium was detected among the MIRU- ***VNTR*** loci in this model. This linkage disequilibrium was also evident when the MIRU- ***VNTR*** types were compared with the IS6110 restriction fragment length polymorphism types. These results support a predominant clonal evolution of M. ***tuberculosis*** .

L8 ANSWER 54 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 11
AN 2004:113829 BIOSIS
DN PREV200400114312
TI Investigations into an outbreak of ***tuberculosis*** in a flock of sheep in contact with ***tuberculous*** cattle.
AU Malone, F. E. [Reprint Author]; Wilson, E. C.; Pollock, J. M.; Skuce, R. A.
CS Veterinary Sciences Division, Department of Agriculture and Rural Development for Northern Ireland, 43 Beltany Road, Omagh, County Tyrone, BT78 5NF, UK
frank.malone@dardni.gov.uk
SO Journal of Veterinary Medicine Series B, (December 2003) Vol. 50, No. 10, pp. 500-504. print.
ISSN: 0931-1793 (ISSN print).
DT Article
LA English
ED Entered STN: 25 Feb 2004
Last Updated on STN: 25 Feb 2004
AB ***Tuberculosis*** , associated with Mycobacterium bovis infection, occurs infrequently in sheep. A sheep flock, which was potentially exposed to a high level of infection from in-contact ***tuberculous*** cattle, was examined for evidence of infection. Six sheep that had given a positive reaction to the comparative intradermal ***tuberculin*** test were examined post mortem. ***Tuberculous*** lesions were present in four of these sheep. Lesion morphology and distribution in the sheep was similar to that in cattle. M. bovis was cultured from the lesions and the isolates were strain typed by spoligotyping and variable number of tandem repeats (***VNTR***) typing. ***Tuberculin*** -reacting sheep also reacted positively to an assay for in vitro release

of interferon-gamma. This paper describes the first report of an outbreak of ***tuberculosis*** in sheep in either Britain or Ireland. The report describes immunology and pathology findings and, using molecular typing techniques, suggests that the sheep had been infected from in-contact cattle.

L8 ANSWER 55 OF 145 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN DUPLICATE 12
AN 2004000801 EMBASE
TI Genotyping in contact investigations: A CDC perspective.
AU Crawford J.T.
CS J.T. Crawford, Ctr. for Dis. Contr. and Prevention, Mailstop F-08, 1600 Clifton Rd, N E, Atlanta, GA 30333, United States. jcrawford@cdc.gov
SO International Journal of Tuberculosis and Lung Disease, (2003) 7/12 SUPPL. 3 (S453-S457).
Refs: 33
ISSN: 1027-3719 CODEN: IJTDFO
CY France
DT Journal; General Review
FS 004 Microbiology
015 Chest Diseases, Thoracic Surgery and Tuberculosis
017 Public Health, Social Medicine and Epidemiology
LA English
SL English
AB Genotyping of Mycobacterium ***tuberculosis*** isolates has been widely used to support investigations of outbreaks and as a tool for studying transmission dynamics and other aspects of ***tuberculosis*** epidemiology. Its applications to contact investigations are more limited. Targeted typing can be used to confirm or disprove suspected relationships among cases. Universal typing of isolates can be used to identify unsuspected transmission and broaden the scope of contact investigations. In order to properly use the results, one must understand the nature of the changes in the M. ***tuberculosis*** genome that produce the heterogeneity reflected in the genotypes, and understand the discriminatory power of the various methods. IS6110 fingerprinting provides the highest discriminatory power, but can be a slow process. Spoligo-typing and MIRU- ***VNTR*** are PCR-based methods that provide faster turnaround and produce digital results that facilitate comparisons. Appropriately used, isolate genotyping can be a useful adjunct to standard contact investigations.

L8 ANSWER 56 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:371207 BIOSIS
DN PREV200300371207
TI Deciphering the population structure of Mycobacterium ***tuberculosis*** using ***VNTR*** -minisatellites.
AU Supply, P. [Reprint Author]; Warren, R. M.; Banuls, A. L.; Lesjean, S. [Reprint Author]; van der Spuy, G. D.; Lewis, L. A.; Tibayrenc, M.; van Helden, P. D.; Locht, C. [Reprint Author]
CS Laboratoire des Mecanismes Moleculaires de la Pathogenese Bacterienne, INSERM U447, Institut Pasteur de Lille, 1, Rue du Prof. Calmette, F-59019, Lille Cedex, France
SO Infection Genetics and Evolution, (April 2003) Vol. 2, No. 4, pp. 267. print.
Meeting Info.: Sixth International Meeting on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases. Paris, France. July 23, 2002-July 27, 2003.
ISSN: 1567-1348 (ISSN print).
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 13 Aug 2003
Last Updated on STN: 13 Aug 2003

L8 ANSWER 57 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2004:33011 BIOSIS
DN PREV200400034253
TI Automated MIRU typing of Mycobacterium ***tuberculosis*** by PCR and WAVE nucleic acid fragment analysis system.
AU Evans, J. T. [Reprint Author]; Hawkey, P. M. [Reprint Author]; Smith, E. G. [Reprint Author]; Hong, G.; Warren, R. E.

CS Health Protection Agency West Midlands, Heartlands Hosp., Birmingham, UK
SO Abstracts of the Interscience Conference on Antimicrobial Agents and Chemotherapy, (2003) Vol. 43, pp. 191. print.
Meeting Info.: 43rd Annual Interscience Conference on Antimicrobial Agents and Chemotherapy. Chicago, IL, USA. September 14-17, 2003. American Society for Microbiology.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 7 Jan 2004
Last Updated on STN: 7 Jan 2004
AB Background: MIRU (Mycobacterial Interspersed Repetitive Unit) typing exhibits similar discrimination to IS6110 RFLP. MIRU typing is a rapid PCR-based method, which is potentially automatable and provides reproducible digital results in the form of a 12-digit allele code. Therefore, real-time typing of strains is possible. Methods: Twenty strains were initially typed using non-denaturing HPLC (WAVE(R) System, Transgenomic, Inc) because this set encompassed the entire range of repeats observed in the West Midlands and had been conventionally typed by ***VNTR*** , MIRU, and IS6110 RFLP. DNA was extracted from strains cultured in Mycobacterial Growth Indicator Tubes via the Qiagen DNA Mini-kit. The 12 MIRU loci were amplified using a novel set of PCR primers and analysed using the non-denaturing double-stranded multiple fragment DNA sizing analysis programme. The retention time of each fragment was converted into fragment size (bp) and the number of tandem DNA repeats at each locus was calculated. Once this preliminary validation was completed, all clinical strains were analysed using WAVE(R) System. Results: Multiple runs were performed on the twenty strains. Agarose gel electrophoresis and WAVE(R) System achieved the same MIRU profiles for each strain. The highest SD of all the fragment sizes was +-8 bp and the largest 95% CI was 10 bp. Each calculated fragment size was within the acceptable SD and 95% CI ranges. MIRU analysis using WAVE(R) System was 100% sensitive, specific and reproducible. Conclusions: The digital format of MIRU profiles enables high-throughput, straightforward comparison of strains. Application of real-time typing has provided clinicians with unknown epidemiological links between patients in a timely manner.

L8 ANSWER 58 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 13
AN 2003:442684 BIOSIS
DN PREV200300442684
TI Genotyping of the Mycobacterium ***tuberculosis*** complex using MIRUs: Association with ***VNTR*** and spoligotyping for molecular epidemiology and evolutionary genetics.
AU Sola, Christophe [Reprint Author]; Filliol, Ingrid; Legrand, Eric; Lesjean, Sarah; Locht, Camille; Supply, Philippe; Rastogi, Nalin
CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur de Guadeloupe, Morne Jolivière, F-97165, BP 484, Pointe-a-Pitre Cedex, Guadeloupe
csola@pasteur-guadeloupe.fr; nrastogi@pasteur-guadeloupe.fr
SO Infection Genetics and Evolution, (July 2003) Vol. 3, No. 2, pp. 125-133. print.
ISSN: 1567-1348 (ISSN print).
DT Article
LA English
ED Entered STN: 24 Sep 2003
Last Updated on STN: 24 Sep 2003
AB The recent introduction of molecular methods has gained increased acceptance as a powerful tool for epidemiology and phylogeny of ***tuberculosis*** (TB). In this investigation, the efficiency of molecular typing using mycobacterial interspersed repetitive units (MIRUs) was assessed on a set of 116 Mycobacterium ***tuberculosis*** complex clinical isolates from 11 different geographic origins. The results obtained were compared with spoligotyping and variable number of tandem DNA repeats (VNTRs) typing data. Eighty-nine different MIRU profiles were obtained on the sample studied. Spoligotyping- or ***VNTR*** -defined clusters were split into subclusters by MIRU typing. Conversely, almost all of the clinical isolates clustered by MIRUs were shown to belong to spoligotyping-based defined clusters. The calculation of the discriminative power by the Hunter-Gaston index (HGI) for ***VNTR*** ,

spoligotyping and MIRU typing gave the values of, respectively, 0.959, 0.965 and 0.988, showing the high discriminative power of the MIRUs. The allelic diversity of the sample was calculated for each of the MIRU- ***VNTR*** loci; five MIRU loci (MIRU nos. 10, 23, 26, 31 and 40) were "highly discriminant", four (MIRU nos. 4, 16, 24 and 39) were "moderately discriminant", and three (MIRU nos. 2, 20 and 27) were "poorly discriminant". Among the three complementary VNTRs (exact tandem repeats ETR-A, ETR-B and ETR-C), ETR-A was the most discriminant locus. A combined numerical analysis of spoligotyping, ***VNTR*** and MIRU typing results partly corroborated a recently hypothesized evolutionary scenario for the M. ***tuberculosis*** complex. M. canettii would be the first branch to have diverged from a common M. ***tuberculosis*** complex ancestor. The East-African Indian (EAI) clade could be the first family to have diverged thereafter. A third branching separated a M. africanum-M. bovis clade, followed by a node separating Beijing versus non-Beijing M. ***tuberculosis*** . The Beijing clade was distinct from the Central Asian 1 (CAS1) family. Among non-Beijing strains, branches such as the Latin-American and Mediterranean (LAM), X and Haarlem clades diverged later. In conclusion, the results obtained show the congruence between clades defined by spoligotyping, and MIRU- ***VNTR*** , and underline the potential of these methods for M. ***tuberculosis*** phylogeny reconstruction. We also conclude that MIRU typing is a very promising method that may be used in a "two PCR-based" genotyping strategy, in conjunction to conventional epidemiological investigations.

L8 ANSWER 59 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 14
AN 2004:85794 BIOSIS
DN PREV200400089055
TI Epidemiology of Mycobacterium bovis infections of pigs and wild boars using a molecular approach.
AU Parra, A. [Reprint Author]; Fernandez-Llario, P.; Tato, A.; Larrasa, J.; Garcia, A.; Alonso, J. M.; Hermoso de Mendoza, M.; Hermoso de Mendoza, J.
CS Catedra de Patologia Infecciosa y Epidemiologia, Departamento de Medicina y Sanidad Animal, Facultad de Veterinaria de Caceres, UEX, Avda. de la Universidad s/n, 10071, Caceres, Spain
aparra@unex.es
SO Veterinary Microbiology, (2 December 2003) Vol. 97, No. 1-2, pp. 123-133. print.
CODEN: VMICDQ. ISSN: 0378-1135.
DT Article
LA English
ED Entered STN: 11 Feb 2004
Last Updated on STN: 11 Feb 2004
AB A molecular epidemiological approach was applied to establishing a possible role for the wild boar as a natural reservoir of Mycobacterium bovis in Sierra de Villuercas, Western Spain; an area free of farmed cattle and wild deer populations. Spoligo and ***VNTR*** typing were used over a three year period to study the epidemiological relationship between the occurrence of bovine ***tuberculosis*** (TB) in extensively bred Iberian pigs and indigenous wild boar. The 37 sampled wild boar showed different degree of calcified granulomatous lesions in retropharyngeal, mediastinal and pulmonary lymph nodes. The 25 sampled Iberian pigs showed calcified lesions, mainly in the respiratory tract. Lesions located in the mesenteric lymph nodes appeared secondarily. M. bovis was isolated from all affected animals. Twenty-five and 37 isolates of M. bovis were obtained from domestic pigs and wild boar, respectively. Our findings provide evidence that supports the possibility of cross infection between wild boar and domestic pig populations. This is contrary to the generally held belief that swine represent an epidemiological dead end host and play no role in the epidemiology of M. bovis.

L8 ANSWER 60 OF 145 CABA COPYRIGHT 2004 CABI on STN
AN 2003:88398 CABA
DN 20033056918
TI Association between molecular type and the epidemiological features of Mycobacterium bovis in cattle
AU Goodchild, A. V.; Rua Domenech, R. de la; Palmer, S.; Dale, J.; Gordon, S. V.; Hewinson, R. G.; Clifton-Hadley, R. S.; de la Rua Domenech, R.; Reid, S. W. J. [EDITOR]; Menzies, F. D. [EDITOR]

CS Epidemiology Dept, Veterinary Laboratories Agency, New Haw, Addlestone, Surrey, KT15 3NB, UK. t.goodchild@vla.defra.gsi.gov.uk

SO Society for Veterinary Epidemiology and Preventive Medicine. Proceedings of a meeting held at University of Warwick, England, 31st March-2nd April 2003, (2003) pp. 45-59. 7 ref.
Publisher: Society for Veterinary Epidemiology and Preventive Medicine. Roslin
Price: Journal article; Conference paper .
Meeting Info.: Society for Veterinary Epidemiology and Preventive Medicine. Proceedings of a meeting held at University of Warwick, England, 31st March-2nd April 2003.
ISBN: 0-948073-59-4

CY United Kingdom

DT Journal

LA English

ED Entered STN: 20030606
Last Updated on STN: 20030606

AB We hypothesized that the molecular type of Mycobacterium bovis is associated with the pathology and epidemiology of the disease in cattle. Analyses are based on spoligotyping (n=11 703 isolates) and ***variable*** ***number*** ***tandem*** ***repeat*** typing (***VNTR*** ; n=1824 isolates), and epidemiological features are calculated from herd, skin test, abattoir and culture data. Spatial confounding was reduced using either polynomial regression on map coordinates, or blocks having diverse spoligotypes. The continuous responses, prevalence of non-visible lesions in the cattle population, incident duration and size of the reaction to avian ***tuberculin*** were significantly affected by spoligotype, while prevalence of non-visible lesions in the cattle population was affected by ***VNTR*** . The binomial responses, proportion of all reactors detected at the disclosing test (DT), proportion of reactors at DT that were inconclusive and proportion of reactors at DT that had visible lesions, were significant in at least five contrasts between molecular types. The effects were consistent with molecular type affecting the specificity of the skin test.

L8 ANSWER 61 OF 145 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

AN 2004200065 EMBASE

TI Molecular typing of Mycobacterium bovis BCG, substrain Sofia SL222, based on variable number of tandem repeats.

AU Stefanova T.; Dale J.; Gordon St.V.

CS T. Stefanova, BCG Laboratory, BulBio-NCIPD, Ltd., 26, Y. Sakazov Blvd., Sofia, Bulgaria

SO Problems of Infectious and Parasitic Diseases, (2003) 31/2 (30-32).
Refs: 8
ISSN: 0204-9155 CODEN: PIPDD4

CY Bulgaria

DT Journal; Article

FS 004 Microbiology

LA English

SL English

AB The availability of the complete genome sequence of Mycobacterium ***tuberculosis*** and its detailed bioinformatic analysis has proved us with a wealth of new information and understanding of the biology of this major human pathogen. Comparative genomics of all members of the M. ***tuberculosis*** complex are beginning to explain differences inhost range and the molecular basis of pathogenicity. Thanks to the recent progress of the molecular genetic the differences has been demonstrated between M. bovis BCG and M. ***tuberculosis*** , between M.bovis BCG and virulent M.bovis as well as genetic distinction between different BCG strains. With the availability of the genome sequence for M. ***tuberculosis*** complex strains novel PCR-based typing method have been proposed, which target variable number tandem repeats (VNTRs) of minisatellite like mycobacterial interspersed repetitive units (MIRUs) or exact tandem repeats (ETRs). The paper describes the results from the typing of Mycobacterium bovis BCG Sofia based on variable number of tandem repeats (***VNTR***) in comparison to another BCG strains currently in use. The tracing of the line Master Seed Lot - Working Seed Lot - Commercial Lots allowed as proving the stability of the product on molecular level for more than 30 years.

L8 ANSWER 62 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:399193 CAPLUS
DN 139:3278
TI Molecular epidemiological manual for Mycobacterium ***tuberculosis*** complex and Mycobacterium avium using ***VNTR*** (variable numbers of tandem repeats) typing
AU Nishimori, Kei; Uchida, Ikuo; Tanaka, Kiyoshi; Nishimori, Tomoko; Imai, Kunitoshi; Kashiwazaki, Yoshihito; Murata, Norihisa; Jinma, Kiyoe
CS Hokkaido Research Station, National Institute of Animal Health, Sapporo, 062-0045, Japan
SO Dobutsu Eisei Kenkyusho Kenkyu Hokoku (2003), Volume Date 2002, 109, 25-32
CODEN: DEKKC9; ISSN: 1347-2542
PB Nogyo Gijutsu Kenkyu Kiko Dobutsu Eisei Kenkyusho
DT Journal; General Review
LA Japanese
AB A review. In order to introduce the new mol. epidemiol. anal. of Mycobacterium ***tuberculosis*** complex and Mycobacterium avium using ***VNTR*** (Variable Nos. of Tandem Repeats) typing, lab. protocols from PCR to phylogenetic anal. are described.

L8 ANSWER 63 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:384593 CAPLUS
TI Molecular-genetic characteristics of rifampicin-resistant Mycobacterium ***tuberculosis*** isolates in Novosibirsk
AU Norkina, O. V.; Filipenko, M. L.; Nikonova, A. A.; Kinsht, V. N.; Kurunov, Yu. N.; Krasnov, V. A.; Tatkov, S. I.
CS Novosib. Inst. Bioorg. Khim., SO RAMN, Russia
SO Problemy Tuberkuleza i Boleznei Legkikh (2003), (12), 22-25
CODEN: PTBLBX; ISSN: 1728-2993
PB Izdatel'stvo Meditsina
DT Journal
LA Russian
AB Forty rifampicin-resistant clin. isolates from patients living in Novosibirsk were studied. Six alleles earlier described in the literature were identified by the sequencing technique. The frequency of mutations in the studied samples slightly differs from that earlier reported for other geog. regions: 21 (52.5%) strains carried the mutated codon TTG in position 531 (Ser .fwdarw. Len), 7 (17.5%) had GTC in position 516 (Asp .fwdarw. Val) and 2 (5%) had the GAC substitution in position 526 (His .fwdarw. Asp), which is prevalent elsewhere. Sequence anal. revealed no mitations in 5 (12.5%) of the 40 isolates although this isolate was repeatedly resistant to rifampicin. ***VNTR*** -typing targeted to tandem repeats (ETR A, B, C, D, and E) was carried out to establish a genetic relationship for rifampicin-resistant isolates. Nine genetic types with ***VNTR*** -profiles termed as 12322, 32122, 32123, 32124, 32125, 32522, 23524, 12223, 22222, 33433 were revealed. There was no strict correlation between the type of mutation in the rpoB gene and the ***VNTR*** -type, which reflects different rates of evolution and the level of selective pressure on these genetic targets. The isolates of ***VNTR*** -types 32123 and 32125 with mutations in codon 531, and type 32122 in codons 531, 526, 516 showed a high clustering. This is likely to reflect the recent transmission and clonal dissemination of the epidemic strains of Mycobacterium ***tuberculosis*** . Thus, mutations in the rpoB gene did not reduce the virulence and transmissivity of these clones. Twenty-six of 27 clin. isolates selected by rifampicin-resistance were also resistant to isoniazid, which confirms the known fact that rifampicin-resistance may be used as a marker of isoniazid-resistance.

L8 ANSWER 64 OF 145 MEDLINE on STN
AN 2004115733 IN-PROCESS
DN PubMed ID: 15004967
TI In Process Citation.
AU Anonymous
SO Problemy tuberkuleza, (2003) (12) 22-5.
Journal code: 0414141. ISSN: 0032-9533.
CY Russia: Russian Federation
DT Journal; Article; (JOURNAL ARTICLE)
LA Russian
FS IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20040310

Last Updated on STN: 20040310

AB Forty rifampicin-resistant clinical isolates from patients living in Novosibirsk were studied. Six alleles earlier described in the literature were identified by the sequencing technique. The frequency of mutations in the studied samples slightly differs from that earlier reported for other geographic regions: 21 (52.5%) strains carried the mutated codon TTG in position 531 (Ser-->Leu), 7 (17.5%) had GTC in position 516 (Asp-->Val) and 2 (5%) had the GAC substitution in position 526 (His-->Asp), which is prevalent elsewhere. Sequence analysis revealed no mitations in 5 (12.5%) of the 40 isolates although this isolate was repeatedly resistant to rifampicin. ***VNTR*** -typing targeted to tandem repeats (ETR A, B, C, D, and E) was carried out to establish a genetic relationship for rifampicin-resistant isolates. Nine genetic types with ***VNTR*** -profiles termed as 12322, 32122, 32123, 32124, 32125, 32522, 23524, 12223, 22222, 33433 were revealed. There was no strict correlation between the type of mutation in the rpoB gene and the ***VNTR*** -type, which reflects different rates of evolution and the level of selective pressure on these genetic targets. The isolates of ***VNTR*** -types 32123 and 32125 with mutations in codon 531, and type 32122 in codons 531, 526, 516 showed a high clustering. This is likely to reflect the recent transmission and clonal dissemination of the epidemic strains of Mycobacterium ***tuberculosis*** . Thus, mutations in the rpoB gene did not reduce the virulence and transmissivity of these clones. Twenty-six of 27 clinical isolates selected by rifampicin-resistance were also resistant to isoniazid, which confirms the known fact that rifampicin-resistance may be used as a marker of isoniazid-resistance.

L8 ANSWER 65 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 15

AN 2003:370218 BIOSIS

DN PREV200300370218

TI Epidemiological study of ***tuberculosis*** in the area of Angers, France, as studied by 3 PCR-based fingerprinting methods.
Original Title: Epidemiologie moleculaire de la ***tuberculose*** dans l'agglomeration angevine etudiee par une strategie d'association de 3 methodes de genotypage par PCR..

AU Sola, C.; Filliol, I.; Maisetti, J.; Carbonnelle, B.; Rastogi, N. [Reprint Author]

CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur de Guadeloupe, Morne Joliviere, 97165, BP 484, Pointe-a-Pitre, Guadeloupe, France
nrastogi@pasteur-guadeloupe.fr

SO Pathologie Biologie, (Fevrier 2003) Vol. 51, No. 1, pp. 13-20. print.
CODEN: PABIAQ. ISSN: 0369-8114.

DT Article

LA French

ED Entered STN: 13 Aug 2003
Last Updated on STN: 13 Aug 2003

AB The new genotyping methods efficiently complement classical epidemiological investigation in order to attempt a global approach to TB control. In the present work, we have studied the genomic diversity of Mycobacterium ***tuberculosis*** isolated during the year 1998 within the district of Angers, France (260,000 inhabitants distributed in 29 districts), in order to identify recent transmission events and any related risk factors. The methods used included "spacer oligonucleotide typing" or spoligotyping, "variable number of DNA tandem repeats" or ***VNTR*** , and "double repetitive element PCR" or DRE-PCR. The resulting spoligotyping and ***VNTR*** results were also feeded to international databases and compared with >10,000 isolates for spoligotyping and 500 isolates for ***VNTR*** , representative of about 60 countries. The results obtained underlined that most of the TB cases in our setting probably reflected reactivation cases, as clustered cases indicative of potential events of recent transmission were rare. Furthermore, interrogation of international databases showed that most of the isolates from the Angers region belonged to major conserved families of TB isolates representative of Europe, with only rare cases of Asian origin, or those previously reported in specific epidemies reported from elsewhere.

L8 ANSWER 66 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 16

AN 2003:466747 BIOSIS
DN PREV200300466747
TI The genetic diversity of Mycobacterium ***tuberculosis*** and an assessment of risk factors (by the method of molecular epidemiology) of ***tuberculosis*** spread in Russia's Siberian region.
AU Norkina, O. V. [Reprint Author]; Kinsht, V. N.; Mokrousov, I. V.; Kurunov, Yu. N.; Krasnov, V. A.; Philipenko, M. L. [Reprint Author]
CS Novosibirsk Research Institute for Bioorganic, Siberia Branch, Chemistry of the Russian Academy of Sciences, Lavrentyev avenue, 8, Novosibirsk, 630090, Russia
SO Molekulyarnaya Genetika Mikrobiologiya i Virusologiya, (2003) No. 3, pp. 9-18. print.
CODEN: MGMVDU. ISSN: 0208-0613.
DT Article
LA Russian
ED Entered STN: 8 Oct 2003
Last Updated on STN: 8 Oct 2003
AB Molecular epidemiology approaches provided for a new interpretation of the TB infection transmission dynamics, contributed to changing the focuses of attention and updated the monitoring practice. On the basis of 101 cases of isolates of Mycobacterium ***tuberculosis*** (MBT) complex sampled from 84 patients with pulmonary ***tuberculosis*** in the Siberian region, we proved that the independent methods of IS6110 RFLP genetic typing and ***VNTR*** -typing by five accurate repeat tandems of ETR A, B, C, D, and E bring about similar results and can be used in studying the MTB clonal structure population in the Siberian region for the purpose of defining the TB infection transmission dynamics. The most widespread genetic types were detected, i.e. Beeijing family strains, the S42 spoligotype, and the 31323 ***VNTR*** type, which account for 52.3% of all samples. The general parameters describing the epidemic process intensity were evaluated, i.e. those characterizing the strains (91.6%) and the transmission activity factor (72%). Consequently, each three of the four analyzed TB cases resulted from a recent transmission. However, there is a trend, within the analyzed samples, towards a higher percentage of clusterization in the age group ranging from 40 to 60. Such trend is typical of a prevalence of TB reactivation cases caused by MBT complex strains spread intensively in the discussed territory. As for the clusterized isolates, which are endemic for the territory, such data should be interpreted as a recent transmission only cautiously. 28.5% of the studied isolates are resistant to anti-TB drugs used in medical practice; and 35.7% of them are resistant to izoniazide and rifampicin, therefore, according to the WHO classification they are considered to be poly-antibiotics-resistant (PAR). No strict associations were found between the spectrum of antibiotics-resistance and any of genotypes, however, 30% of PAR strains are 32525 and 42525 types ***VNTR*** (spoligotype S1 or Beejing type).

L8 ANSWER 67 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:529835 BIOSIS
DN PREV200300533397
TI Molecular typing of of Mycobacterium ***tuberculosis*** using variable number tandem repeats based on mycobacterial interspersed repetitive units alone and in association with exact tandem repeats.
AU Kee, S. J. [Reprint Author]; Pyo, H. W. [Reprint Author]; Cho, D. [Reprint Author]; Shin, J. H. [Reprint Author]; Suh, S. P. [Reprint Author]; Ryang, D. W. [Reprint Author]
CS Chonnam National University Hospital, Gwangju, South Korea
SO Abstracts of the General Meeting of the American Society for Microbiology, (2003) Vol. 103, pp. C-238. http://www.asmusa.org/mtgsrc/generalmeeting.htm. cd-rom.
Meeting Info.: 103rd American Society for Microbiology General Meeting. Washington, DC, USA. May 18-22, 2003. American Society for Microbiology. ISSN: 1060-2011 (ISSN print).
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 12 Nov 2003
Last Updated on STN: 12 Nov 2003
AB Background: Mycobacterial interspersed repetitive unit (MIRU) and exact tandem repeat (ETR) genes are most commonly used for ***VNTR*** typing of Mycobacterium ***tuberculosis*** . The purpose of this study was to

evaluate both MIRU- ***VNTR*** and ETR- ***VNTR*** typing methods based on typability, reproducibility, Hunter-Gaston discriminative index (HGI), and clinical usefulness. Methods: We undertook a retrospective study of 119 M. ***tuberculosis*** isolates (97 patients) collected in our hospital from Mar 2000 to Feb 2001. Twelve MIRU loci and five ETR loci were amplified to determine ***VNTR*** profiles for MIRU and ETR, respectively. Results: The results were summarized. MIRU- ***VNTR*** produced more distinct types (n=53) compared to ETR- ***VNTR*** (n=21). The combination of two ***VNTR*** methods generated 57 distinct patterns identifying 40 unique isolates and 79 isolates in 17 individual clusters (A to R). Both ***VNTR*** methods were 100% reproducible for a set of 40 isolates sequentially obtained from 18 patients. The MIRU- ***VNTR*** method identified 24 epidemiologically related M. ***tuberculosis*** isolates in B(10/16), C(2/3), E(5/5), F(5/20) and P(2/5) groups. Among these 24 isolates, 19 except for E group were AFB-smear negative and only one-culture positive and thus were confirmed to be false-positive because each sample group was processed on the same day or consecutive days, together with one or more smear- and culture positive isolates, and all were not compatible with clinical characteristics of ***tuberculosis*** . Five isolates in E group obtained from 2 patients were confirmed to be transmission of the same strain of M. ***tuberculosis*** because of the same residency. The typabilities of MIRU- ***VNTR*** , ETR- ***VNTR*** , and combined ***VNTR*** methods on 77 isolates without known epidemiological links were 68.8%, 27.2%, and 74.0%, respectively. The HGIs of MIRU- ***VNTR*** , ETR- ***VNTR*** , and combined ***VNTR*** methods on 77 isolates without known epidemiological links were 0.982, 0.775, and 0.986, respectively. Conclusion: The results confirmed the potential utility of MIRU- ***VNTR*** typing of identifying cross-contamination and transmission.

L8 ANSWER 68 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:556252 BIOSIS
DN PREV200300556963
TI Evaluation of a strategy for the universal genotyping of Mycobacterium ***tuberculosis*** isolates in the United States.
AU Diem, L. [Reprint Author]; Cowan, L. S. [Reprint Author]; Monson, T.; Oemig, T. O.; Wand, P. J.; Metchock, B. [Reprint Author]; Crawford, J. T. [Reprint Author]
CS Centers for Disease Control and Prevention, Atlanta, GA, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2003) Vol. 103, pp. U-020. http://www.asmusa.org/mtgsrc/generalmeeting.htm. cd-rom.
Meeting Info.: 103rd American Society for Microbiology General Meeting. Washington, DC, USA. May 18-22, 2003. American Society for Microbiology. ISSN: 1060-2011 (ISSN print).
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 26 Nov 2003
Last Updated on STN: 26 Nov 2003
AB Background: To provide universal genotyping of Mycobacterium ***tuberculosis*** isolates in the United States, high-throughput methods are needed to replace the lengthy and laborious IS6110 RFLP method. This study evaluated the proposed strategy of genotyping all isolates using PCR-based methods - spoligotyping and MIRU- ***VNTR*** typing - followed by IS6110 RFLP on clustered isolates only. Methods: Isolates (185) were from an on going, universal typing study in Wisconsin. The isolates were genotyped by spoligotyping, MIRU- ***VNTR*** typing, and IS6110 RFLP Results: The combination of spoligotyping and MIRU- ***VNTR*** typing clustered 47 (25%) isolates into 18 clusters; 25 of these isolates (8 clusters) remained clustered after IS6110 typing. The results also demonstrated the added value of MIRU- ***VNTR*** typing. The combination of spoligotyping and IS6110 RFLP clustered 44 isolates, but 19 of these were distinct by MIRU- ***VNTR*** ; 14 were low-copy number (<6 copies of IS6110) and 5 were high-copy number isolates. The non-specific clustering of isolates by IS6110 with low copy numbers is well documented, but identical high-copy IS6110 patterns are considered to be an indicator of recent transmission. The demographics of patients in clusters defined by identical high-copy number IS6110 RFLP patterns, identical spoligotypes, and different MIRU- ***VNTR*** types were

investigated. There was no evidence to indicate possible transmission links, suggesting that MIRU- ***VNTR*** typing correctly identified these strains as different. We also examined clusters with identical MIRU- ***VNTR*** patterns and related IS6110 patterns (plus or minus one band). Within each of these clusters, all of the isolates had identical spoligotypes, suggesting that spoligotyping did not differentiate related isolates in this study. Conclusion: With the results of this study, the proposed universal typing strategy appears feasible. Spoligotyping and MIRU- ***VNTR*** typing reduced the number of isolates requiring IS6110 fingerprinting by 75%, and because the results of the PCR-based assays can be obtained within 48 hours, the turnaround time for the majority of the isolates is significantly decreased.

L8 ANSWER 69 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:556261 BIOSIS
DN PREV200300556972
TI Identification of Mycobacterium species and characterization of strains using a labchip (microfluidic) instrument.
AU Cooksey, R. C. [Reprint Author]; Limor, J. R. [Reprint Author]
CS CDC, Atlanta, GA, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2003) Vol. 103, pp. U-029. http://www.asmusa.org/mtgsrc/generalmeeting.htm. cd-rom.
Meeting Info.: 103rd American Society for Microbiology General Meeting. Washington, DC, USA. May 18-22, 2003. American Society for Microbiology. ISSN: 1060-2011 (ISSN print).
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 26 Nov 2003
Last Updated on STN: 26 Nov 2003
AB We developed schemes for rapid identification of Mycobacterium species and strain typing using a labchip instrument (Agilent Model 2100 Bioanalyzer) which uses electrokinetic forces to drive samples through chip microchannels (microfluidics), enabling real-time resolution and detection of sample components. A 439-bp region of hsp65 that has sequence polymorphisms specific for most mycobacterial species has been characterized by PCR restriction analysis (PRA) with BstEII or HaeIII as a species identification tool. We performed PRA in duplicate, using 2 strains each of 13 species, and analyzing 1 ul of each digest. Fragment sizes (bp) determined automatically by the instrument were consistently smaller than the correct sizes for each of the species as determined by sequence analysis (mean variance, 7.5%) but varied by ltoreq6 bp for specific fragments in duplicate runs. M. ***tuberculosis*** isolates were typed with the labchip instrument by using mycobacterial interspersed repetitive unit (MIRU) typing, a ***variable*** ***number*** ***tandem*** ***repeat*** typing method which determines the number of copies of repeated units at 12 loci scattered throughout the genome based on product size after PCR amplification. Eleven isolates with 1 to 6 repeat copies at each locus were examined. Sizes were smaller by a mean of 4% compared to correct sizes predicted by sequence analysis, varied on duplicate runs by ltoreq5 bp, and could be used to correctly identify all strain types. Nontuberculous Mycobacterium species were typed using randomly amplified polymorphic DNA (RAPD) electrophoresis on the labchip instrument. PCR using a single 10-mer primer and low annealing temperature (37degreeC) was performed using 5 clusters each of M. chelonae, M. abscessus, and M. mucogenicum (13 isolates of each species) and 3 clusters of M. avium (11 isolates). All clusters were distinguished when patterns were compared to results of pulsed-field gel electrophoresis. RAPD patterns for 1 M. abscessus strain were unchanged when we tested DNA from 2 cultures or DNA extracted on 6 different days from the same culture. The labchip instrument is a versatile alternative for sizing mycobacterial DNA fragments.

L8 ANSWER 70 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:556264 BIOSIS
DN PREV200300556975
TI Evaluation of variable-number tandem repeats (VNTRs) of mycobacterial interspersed repetitive units (MIRUs) for genotyping of M. ***tuberculosis*** strains in respiratory samples.

AU Mondo, A. [Reprint Author]; Pittaluga, F.; Piana, F.; Cirillo, D.; Chirillo, M. G.; Milano, R.; Fabbro, L.; Bugiani, M.; Bonora, S. [Reprint Author]; Di Perri, G. [Reprint Author]
CS University of Turin, Torino, Italy
SO Abstracts of the General Meeting of the American Society for Microbiology, (2003) Vol. 103, pp. U-032. http://www.asmusa.org/mtgsrc/generalmeeting.htm. cd-rom.
Meeting Info.: 103rd American Society for Microbiology General Meeting. Washington, DC, USA. May 18-22, 2003. American Society for Microbiology. ISSN: 1060-2011 (ISSN print).
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 26 Nov 2003
Last Updated on STN: 26 Nov 2003
AB Background: The current golden standard of M. ***tuberculosis*** genotyping, IS6110-Restriction Fragment Length Polymorphism, shows a delay in obtaining results due to the need of culture-derived large amounts of high-purified chromosomal DNA. MIRU- ***VNTR*** has been recently identified as a new PCR-based technique for genotyping of M. ***tuberculosis*** strains. It relies on the strain-specific variability of the genetic elements named MIRUs in 12 human minisatellite-like regions of the M. ***tuberculosis*** genome and appears to be a rapid and portable approach to molecular epidemiology of ***tuberculosis*** . The aim of our study is to evaluate the use of MIRU- ***VNTR*** with DNA extracted directly from clinical respiratory specimens. Methods: Chromosomal DNA was extracted with an alkaline lysis-based method from 12 acid fast bacilli (AFB)-smear positive sputum samples (ranging from + to +++ according to the WHO), after standard decontamination and concentration. MIRU- ***VNTR*** was performed both with these samples and correspondent phenol-chloroform extracted DNAs obtained from growth in culture, and results were compared. PCR was performed according to Supply et al. (Mol Biol 2000, 36: 762-771), and H37-Rv strain was used as a positive control. Results: All the 12 sputum-derived samples showed a clear signal of amplification for all the 12 MIRUs. The comparison of PCR results between these samples and culture-derived DNA samples showed identical patterns for all the strains. Conclusion: MIRU- ***VNTR*** performed with AFB-positive respiratory samples showed to be a rapid and simple PCR-based method to genotype M. ***tuberculosis*** strains, supplying the results in advance compared to than obtained from culture-derived samples. This approach could be useful in the case of ongoing outbreaks (i.e. in nosocomial setting), especially to survey the spread of drug-resistant strains, or to design genotyping studies where culture is not regularly available (i.e. developing countries). Moreover, MIRU- ***VNTR*** positivity, although without any diagnostic value, confirms in advance the identification of the AFB observed in the smear as mycobacteria belonging to M. ***tuberculosis*** complex.

L8 ANSWER 71 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 17
AN 2002:221150 CAPLUS
DN 136:259533
TI Methods and systems for molecular fingerprinting using microfabricated flow devices for fractionation of nucleic acids
IN Quake, Stephen R.; Chou, Hou-pu
PA California Institute of Technology, Inc., USA
SO U.S. Pat. Appl. Publ., 49 pp., Cont.-in-part of U. S. Ser. No. 325,667.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2002034748	A1	20020321	US 2001-826373	20010404
	US 6540895	B1	20030401	US 1999-325667	19990521
PRAI	US 1997-932774	A2	19970923		
	US 1999-325667	A2	19990521		
	US 2000-194422P	P	20000404		
	US 1998-86394P	P	19980522		
	US 1998-108894P	P	19981117		

AB This invention relates in general to a method for mol. fingerprinting.

The method can be used for forensic identification (e.g. DNA fingerprinting, esp. by ***VNTR***), bacterial typing, and human/animal pathogen diagnosis. More particularly, mols. such as polynucleotides (e.g. DNA) can be assessed or sorted by size in a microfabricated device that analyzes the polynucleotides according to restriction fragment length polymorphism. In a microfabricated device according to the invention, DNA fragments or other mols. can be rapidly and accurately typed using relatively small samples, by measuring for example the signal of an optically-detectable (e.g., fluorescent) reporter assocd. with the polynucleotide fragments.

L8 ANSWER 72 OF 145 USPATFULL on STN
AN 2002:300840 USPATFULL
TI Modifications of antigens by the introduction of aldehyde groups and their use in enhancing the immune response
IN Fearon, Douglas T., Cambridge, UNITED KINGDOM
Allison, Michael, Cambridge, UNITED KINGDOM
PA Cambridge University Technical Services Limited (non-U.S. corporation)
PI US 2002168383 A1 20021114
AI US 2001-994858 A1 20011128 (9)
RLI Continuation of Ser. No. US 2000-673725, filed on 20 Oct 2000, PENDING
PRAI GB 1998-8485 19980421
WO 1999-GB1206 19990421
DT Utility
FS APPLICATION
LREP NIXON & VANDERHYE P.C., 1100 North Glebe Road, 8th Floor, Arlington, VA, 22201-4714
CLMN Number of Claims: 10
ECL Exemplary Claim: 1
DRWN 16 Drawing Page(s)
LN.CNT 737
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides a method of producing an immune response in a mammal to an antigen which comprises modifying said antigen by introducing an alkyl aldehyde group into said antigen and introducing said modified antigen into the mammal. Periodate or glycolaldhyde may be used as the agent to introduce the aldehyde groups.

L8 ANSWER 73 OF 145 USPATFULL on STN
AN 2002:287639 USPATFULL
TI Recombinant BCG vaccines for the prevention and treatment of cancer
IN Chung, Maureen Angela, Providence, RI, UNITED STATES
Sharma, Surendra, Warwick, RI, UNITED STATES
O'Donnell, Michael Alan, Iowa City, IA, UNITED STATES
Chang, Helena R., Los Angeles, CA, UNITED STATES
PA Roger Williams Hospital, Providence, RI (U.S. corporation)
PI US 2002160502 A1 20021031
AI US 2001-965131 A1 20010926 (9)
PRAI US 2000-235455P 20000926 (60)
DT Utility
FS APPLICATION
LREP LAHIVE & COCKFIELD, 28 STATE STREET, BOSTON, MA, 02109
CLMN Number of Claims: 36
ECL Exemplary Claim: 1
DRWN 6 Drawing Page(s)
LN.CNT 1842
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to recombinant mycobacteria, particularly recombinant M. bovis, BCG, engineered to express a MUC1 polypeptide and human interleukin-2 for use in cancer immunotherapy.

L8 ANSWER 74 OF 145 USPATFULL on STN
AN 2002:272782 USPATFULL
TI Diagnostics based on mass spectrometry
IN Koster, Hubert, La Jolla, CA, UNITED STATES
PI US 2002150903 A1 20021017
US 6589485 B2 20030708
AI US 2001-879341 A1 20010611 (9)
RLI Continuation of Ser. No. US 2001-786416, filed on 11 Oct 2001, PENDING
Continuation of Ser. No. US 2000-495444, filed on 31 Jan 2000, GRANTED, Pat. No. US 6300076 Continuation of Ser. No. US 2000-504245, filed on 15

Feb 2000, GRANTED, Pat. No. US 6221605 Continuation of Ser. No. US 1999-287679, filed on 6 Apr 1999, GRANTED, Pat. No. US 6258538 Continuation of Ser. No. US 1996-617256, filed on 18 Mar 1996, GRANTED, Pat. No. US 6043031 Continuation-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995, GRANTED, Pat. No. US 5605798
DT Utility
FS APPLICATION
LREP Stephanie Seidman, Heller Ehrman White & McAuliffe LLP, 6th Floor, 4350 La Jolla Village Drive, San Diego, CA, 92122-1246
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 57 Drawing Page(s)
LN.CNT 2636
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting particular nucleic acid molecules and sequences in the molecules are provided. Arrays of oligonucleotides for performing mass spectrometric analyses are provided.

L8 ANSWER 75 OF 145 USPATFULL on STN
AN 2002:272775 USPATFULL
TI Methods of treatment of type 2 diabetes
IN Polonsky, Kenneth S., Chicago, IL, UNITED STATES
Horikawa, Yukio, Kobe City, JAPAN
Oda, Naohisa, Nagoya-shi, JAPAN
Cox, Nancy J., Inverness, IL, UNITED STATES
Otani, Kenichi, Chicago, IL, UNITED STATES
Hanis, Craig L., Houston, TX, UNITED STATES
Bell, Graeme I., Chicago, IL, UNITED STATES
Sreenan, Seamus Kevin, Dublin 3, IRELAND
Zhou, Yun-Ping, Pleasanton, CA, UNITED STATES
PA Board of Regents, The University of Texas System (U.S. corporation)
PI US 2002150896 A1 20021017
AI US 2001-768877 A1 20010123 (9)
RLI Division of Ser. No. US 1999-422869, filed on 21 Oct 1999, GRANTED, Pat. No. US 6235481
PRAI US 1998-105052P 19981021 (60)
US 1999-134175P 19990513 (60)
DT Utility
FS APPLICATION
LREP Gina N. Shishima, FULBRIGHT & JAWORSKI L.L.P., Suite 2400, 600 Congress Avenue, Austin, TX, 78701
CLMN Number of Claims: 48
ECL Exemplary Claim: 1
DRWN 26 Drawing Page(s)
LN.CNT 8520
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates generally to the field of diabetes. More particularly, it concerns the identification of genes responsible for NIDDM1 for use in diagnostic and therapeutic applications. The present invention demonstrates that the NIDDM1 locus is, in fact, the calpain 10 gene. The invention further relates to the discovery that analysis of mutations in calpain genes and gene products can be diagnostic for type 2 diabetes. The invention also contemplates methods of treating diabetes in view of the fact that calpain mutations can cause diabetes. Further, the invention relates to novel polynucleotides of the NIDDM1 locus and polypeptides encoded by such polynucleotides.

L8 ANSWER 76 OF 145 USPATFULL on STN
AN 2002:272771 USPATFULL
TI DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTILIZE THE T CELL RECEPTOR BETA GENE REGION
IN HOOD, LEROY E., SEATTLE, WA, UNITED STATES
ROWEN, LEE, SEATTLE, WA, UNITED STATES
PI US 2002150891 A1 20021017
AI US 1999-263959 A1 19990305 (9)
RLI Continuation of Ser. No. US 1995-531241, filed on 19 Sep 1995, ABANDONED Continuation-in-part of Ser. No. US 1994-309335, filed on 19 Sep 1994, ABANDONED
DT Utility
FS APPLICATION

LREP Jane E. R. Potter, Esq., Seed Intellectual Property Law Group PLLC, 701 fifth Avenue,, Suite 6300, Seattle, WA, 98104-7092
CLMN Number of Claims: 18
ECL Exemplary Claim: 1
DRWN 133 Drawing Page(s)
LN.CNT 3258
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides isolated nucleic acid molecules encoding a variety of V.beta. genes (e.g., V.beta.25, V.beta.26, V.beta.27, V.beta.28, V.beta.29, V.beta.30 or V.beta.31) as well as both 5' and 3' sequences which flank a T cell receptor .beta. gene. Also provided are kits of primers and kits of antibodies. Further, the present invention also provides methods for diagnosing organ transplant rejection, as well as methods for determining a correlation between a disease or disease susceptibility and a selected polymorphism.

L8 ANSWER 77 OF 145 USPATFULL on STN
AN 2002:251102 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, La Jolla, CA, UNITED STATES
PI US 2002137046 A1 20020926
US 6500621 B2 20021231
AI US 2001-796416 A1 20010228 (9)
RLI Continuation of Ser. No. US 2000-495444, filed on 31 Jan 2000, GRANTED, Pat. No. US 6300076 Continuation of Ser. No. US 2000-504245, filed on 15 Feb 2000, GRANTED, Pat. No. US 6221605 Continuation of Ser. No. US 1996-617256, filed on 18 Mar 1996, GRANTED, Pat. No. US 6043031 Continuation of Ser. No. US 1995-406199, filed on 17 Mar 1995, GRANTED, Pat. No. US 5605798 Continuation of Ser. No. US 1999-287679, filed on 6 Apr 1999, GRANTED, Pat. No. US 6258538
DT Utility
FS APPLICATION
LREP STEPHANIE L. SEIDMAN, ESQ., HELLER EHRMAN WHITE & MCAULIFFE LLP, 6TH FLOOR, 4350 LA JOLLA VILLAGE DRIVE, SAN DIEGO, CA, 92122-1246
CLMN Number of Claims: 21
ECL Exemplary Claim: 1
DRWN 57 Drawing Page(s)
LN.CNT 2632
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting particular nucleic acid molecules and sequences in the molecules are provided. Depending upon the sequence to be detected, the processes, for example, can be used to diagnose a genetic disease or a chromosomal abnormality, a predisposition to a disease or condition, or infection by a pathogen, or for determining identity or heredity.

L8 ANSWER 78 OF 145 USPATFULL on STN
AN 2002:198633 USPATFULL
TI Fatty acid transport proteins
IN Stahl, Andreas, Allston, MA, UNITED STATES
Hirsch, David J., Brookline, MA, UNITED STATES
Lodish, Harvey F., Brookline, MA, UNITED STATES
PA Whitehead Institute for Biomedical Research, Cambridge, MA, UNITED STATES (U.S. corporation)
PI US 2002106733 A1 20020808
AI US 2001-943671 A1 20010831 (9)
RLI Division of Ser. No. US 1999-232191, filed on 14 Jan 1999, PATENTED
PRAI US 1998-71374P 19980115 (60)
US 1998-93491P 19980720 (60)
US 1998-110941P 19981204 (60)
DT Utility
FS APPLICATION
LREP HAMILTON, BROOK, SMITH & REYNOLDS, P.C., 530 VIRGINIA ROAD, P.O. BOX 9133, CONCORD, MA, 01742-9133
CLMN Number of Claims: 54
ECL Exemplary Claim: 1
DRWN 33 Drawing Page(s)
LN.CNT 3559
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A family of fatty acid transport proteins (FATPs) mediate transport of long chain fatty acids (LCFAs) across cell membranes into cells. These

proteins exhibit different expression patterns among the organs of mammals. Nucleic acids encoding FATPs of this family, are described. Also described are methods to test FATPs for fatty acid transport function, and methods to identify inhibitors or enhancers of transport function. The altering of LCFA uptake by administering to the mammal an inhibitor or enhancer of FATP transport function of a FATP can decrease or increase calories available as fats, and can decrease or increase circulating fatty acids. The organ specificity of FATP distribution can be exploited in methods to direct drugs, diagnostic indicators and so forth to an organ.

L8 ANSWER 79 OF 145 USPATFULL on STN
AN 2002:78458 USPATFULL
TI DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
IN KOSTER, HUBERT, LA JOLLA, CA, UNITED STATES
LITTLE, DANIEL P., BOSTON, MA, UNITED STATES
BRAUN, ANDREAS, SAN DIEGO, CA, UNITED STATES
LOUGH, DAVID M., BERWICKSHIRE, UNITED KINGDOM
XIANG, GUOBING, SAN DIEGO, CA, UNITED STATES
VAN DEN BOOM, DIRK, HAMBURG, GERMANY, FEDERAL REPUBLIC OF
JURINKE, CHRISTIAN, HAMBURG, GERMANY, FEDERAL REPUBLIC OF
RUPPERT, ANDREAS, LINDEN, GERMANY, FEDERAL REPUBLIC OF
PI US 2002042112 A1 20020411
AI US 1998-179536 A1 19981026 (9)
RLI Continuation of Ser. No. WO 1997-US20444, filed on 6 Nov 1997, UNKNOWN Continuation-in-part of Ser. No. US 1996-744481, filed on 6 Nov 1996, PENDING Continuation-in-part of Ser. No. US 1996-744590, filed on 6 Nov 1996, GRANTED, Pat. No. US 6074823 Continuation-in-part of Ser. No. US 1996-746036, filed on 6 Nov 1996, GRANTED, Pat. No. US 5900481 Continuation-in-part of Ser. No. US 1996-746055, filed on 6 Nov 1996, ABANDONED Continuation-in-part of Ser. No. US 1997-786988, filed on 23 Jan 1997, PENDING Continuation-in-part of Ser. No. US 1997-787639, filed on 23 Jan 1997, GRANTED, Pat. No. US 6024925 Continuation-in-part of Ser. No. US 1997-933792, filed on 19 Sep 1997, GRANTED, Pat. No. US 6133436 Continuation-in-part of Ser. No. US 1997-947801, filed on 8 Oct 1997, PENDING
DT Utility
FS APPLICATION
LREP HELLER EHRMAN WHITE & MCAULIFFE LLP, 4250 EXECUTIVE SQ, 7TH FLOOR, LA JOLLA, CA, 92037
CLMN Number of Claims: 80
ECL Exemplary Claim: 1
DRWN 123 Drawing Page(s)
LN.CNT 9951
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting a particular nucleic acid sequence in a biological sample are provided. Depending on the sequence to be detected, the processes can be used, for example, to diagnose a genetic disease or chromosomal abnormality; a predisposition to a disease or condition, infection by a pathogenic organism, or for determining identity or heredity.

L8 ANSWER 80 OF 145 USPATFULL on STN
AN 2002:209740 USPATFULL
TI Transgenic models of inflammatory disease
IN Duff, Gordon W., Sheffield, UNITED KINGDOM
Nicklin, Martin, Sheffield, UNITED KINGDOM
PA Interleukin Genetics Inc., Waltham, MA, United States (U.S. corporation)
PI US 6437216 B1 20020820
WO 9925857 19990527
AI US 2001-647826 20010312 (9)
WO 1998-US24287 19981113
20010312 PCT 371 date
PRAI GB 1997-23835 19971113
DT Utility
FS GRANTED
EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Schnizer, Richard
LREP Arnold, Beth E., Quisel, John D., Foley Hoag, LLP
CLMN Number of Claims: 21
ECL Exemplary Claim: 1
DRWN 6 Drawing Figure(s); 6 Drawing Page(s)

LN.CNT 3230
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present provides a mammal in which the expression of one or more interleukin genes has been suppressed. More specifically, the invention concerns the inactivating deletion of the interleukin-1 receptor antagonist gene to produce a knock-out non-human mammal with decreased or completely suppressed expression of the endogenous gene. The invention provides methods for preparing such knock-out mammals and methods of using the knock-out mammals to evaluate the effectiveness of therapeutic agents and regimens to treat diseases or disorders associated with perturbations in the interleukin pathways.

L8 ANSWER 81 OF 145 USPATFULL on STN
AN 2002:194695 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, Concord, MA, United States
Tang, Kai, Brighton, MA, United States
Fu, Dong-Jing, San Diego, CA, United States
Siegert, Carsten W., Hamburg, GERMANY, FEDERAL REPUBLIC OF
Little, Daniel P., San Diego, CA, United States
Braun, Andreas, San Diego, CA, United States
Darnhofer-Demar, Brigitte, Hamburg, GERMANY, FEDERAL REPUBLIC OF
Jurinke, Christian, Hamburg, GERMANY, FEDERAL REPUBLIC OF
Van den Boom, Dirk, Dreieich, GERMANY, FEDERAL REPUBLIC OF
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6428955 B1 20020806
AI US 1996-744481 19961106 (8)
RLI Continuation-in-part of Ser. No. US 1996-617256, filed on 18 Mar 1996
Continuation-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995
DT Utility
FS GRANTED
EXNAM Primary Examiner: Campbell, Eggerton A.
LREP Seidman, Stephanie L., Heller Ehrman White & McAuliffe LLP
CLMN Number of Claims: 18
ECL Exemplary Claim: 1
DRWN 140 Drawing Figure(s); 88 Drawing Page(s)
LN.CNT 4684
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides fast and highly accurate mass spectrometer based processes for detecting a particular nucleic acid sequence in a biological sample. Depending on the sequence to be detected, the processes can be used, for example, to diagnose a genetic disease or chromosomal abnormality; a predisposition to a disease or condition, infection by a pathogenic organism, or for determining identity or heredity.

L8 ANSWER 82 OF 145 USPATFULL on STN
AN 2002:108823 USPATFULL
TI Mass spectrometric detection of polypeptides
IN Little, Daniel, Boston, MA, United States
Koster, Hubert, La Jolla, CA, United States
Higgins, G. Scott, Paisley, UNITED KINGDOM
Lough, David, Berwickshire, UNITED KINGDOM
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6387628 B1 20020514
AI US 2000-664977 20000918 (9)
RLI Division of Ser. No. US 1998-146054, filed on 2 Sep 1998
Continuation-in-part of Ser. No. US 1997-922201, filed on 2 Sep 1997
DT Utility
FS GRANTED
EXNAM Primary Examiner: Campbell, Eggerton A.
LREP Heller Ehrman White & McAuliffe
CLMN Number of Claims: 38
ECL Exemplary Claim: 1
DRWN 3 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 4716
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A process for determining the identity of a target polypeptide using mass spectroscopy is provided. Depending on the target polypeptide to be identified, a process as disclosed can be used, for example, to diagnose a genetic disease or chromosomal abnormality, a predisposition to a

disease or condition, or infection by a pathogenic organism; or for determining identity or heredity. Kits for performing the disclosed processes also are provided.

L8 ANSWER 83 OF 145 USPATFULL on STN
AN 2002:34304 USPATFULL
TI Methods of identifying agents inhibiting fatty acid transport proteins
IN Stahl, Andreas, Allston, MA, United States
Hirsch, David J., Brookline, MA, United States
Lodish, Harvey F., Brookline, MA, United States
Gimeno, Ruth E., Wellesley, MA, United States
Tartaglia, Louis A., Newton, MA, United States
PA Whitehead Institute for Biomedical Research, Cambridge, MA, United States (U.S. corporation)
Millennium Pharaceuticals, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 6348321 B1 20020219
AI US 1999-232201 19990114 (9)
PRAI US 1998-71374P 19980115 (60)
US 1998-93491P 19980720 (60)
US 1998-110941P 19981204 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Kunz, Gary L.; Assistant Examiner: Hamud, Fozia
LREP Hamilton, Brook, Smith & Reynolds, P.C.
CLMN Number of Claims: 80
ECL Exemplary Claim: 1
DRWN 201 Drawing Figure(s); 169 Drawing Page(s)
LN.CNT 9655
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A family of fatty acid transport proteins (FATPS) mediate transport of long chain fatty acids (LCFAs) across cell membranes into cells. These proteins exhibit different expression patterns among the organs of mammals. Nucleic acids encoding FATPs of this family, vectors comprising these nucleic acids, as well as the production of FATP proteins in host cells are described. Also described are methods to test FATPs for fatty acid transport function, and methods to identify inhibitors or enhancers of transport function. The altering of LCFA uptake by administering to the mammal an inhibitor or enhancer of FATP transport function of a FATP in the small intestine can decrease or increase calories available as fats, and can decrease or increase circulating fatty acids. The organ specificity of FATP distribution can be exploited in methods to direct drugs, diagnostic indicators and so forth to an organ such as the heart.

L8 ANSWER 84 OF 145 USPATFULL on STN
AN 2002:29244 USPATFULL
TI Human carbamyl phosphate synthetase I polymorphism and diagnostic methods related thereto
IN Summar, Marshall L., Brentwood, TN, United States
Christman, Brian W., Nashville, TN, United States
PA Vanderbilt University, Nashville, TN, United States (U.S. corporation)
PI US 6346382 B1 20020212
AI US 1999-323472 19990601 (9)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Myers, Carla J.; Assistant Examiner: Johannsen, Diana
LREP Jenkins & Wilson, P.A.
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN 12 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 4874
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Isolated polynucleotide molecules and peptides encoded by these molecules are used in the analysis of human carbamyl phosphate synthetase I phenotypes, as well as in diagnostic and therapeutic applications, relating to a human carbamyl phosphate synthetase I polymorphism. By analyzing genomic DNA or amplified genomic DNA, or amplified cDNA derived from mRNA, it is possible to type a human carbamyl phosphate synthetase I with regard to the human carbamyl phosphate synthetase I polymorphism, for example, in the context of diagnosing and treating hepatic veno-occlusive disease (HVOD) associated

with bone marrow transplants.

L8 ANSWER 85 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 18
AN 2002:968323 CAPLUS
DN 138:249680
TI Stability of variable-number tandem repeats of mycobacterial interspersed repetitive units from 12 loci in serial isolates of Mycobacterium ***tuberculosis***
AU Savine, Evgueni; Warren, Robin M.; van der Spuy, Gian D.; Beyers, Nulda; van Helden, Paul D.; Locht, Camille; Supply, Philip
CS Laboratoire des Mecanismes Moleculaires de la Pathogenese Bacterienne, INSERM U447, Institut Pasteur de Lille, Lille, F-59019, Fr.
SO Journal of Clinical Microbiology (2002), 40(12), 4561-4566
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Variable no. tandem repeats (VNTRs) of elements named mycobacterial interspersed repetitive units (MIRUs) have previously been identified in 12 minisatellite loci of the Mycobacterium ***tuberculosis*** genome. These markers allow reliable high-throughput genotyping of M. ***tuberculosis*** and represent a portable approach to global mol. epidemiol. of M. ***tuberculosis*** . To assess their temporal stability, we genotyped 123 serial isolates, sepd. by up to 6 yr and belonging to a variety of distinct IS6110 restriction fragment length polymorphism (RFLP) families, from 56 patients who had pos. sputum cultures. All 12 MIRU ***VNTR*** loci were completely identical within the groups of serial isolates in 55 out of 56 groups (98.2%), although 11 pairs of isolates from the same patients with conserved MIRU VNTRs displayed slightly different IS6110 RFLP profiles. In a single case, serial isolates with an unchanged IS6110 RFLP profile showed a change in 1 out of 12 MIRU ***VNTR*** loci. These results indicate that MIRU VNTRs are stable over time and therefore are suitable for reliable follow-up of patients chronically infected with ***tuberculosis*** over long periods. Moreover, they support MIRU ***VNTR*** genotyping as a powerful first-line method followed by subtyping by IS6110 RFLP to define ongoing transmission clusters.
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 86 OF 145 CABA COPYRIGHT 2004 CABI on STN DUPLICATE 19
AN 2002:148356 CABA
DN 20023103044
TI Development of ***variable*** - ***number*** ***tandem*** ***repeat*** typing of Mycobacterium bovis: comparison of results with those obtained by using existing exact tandem repeats and spoligotyping
AU Roring, S.; Scott, A.; Brittain, D.; Walker, I.; Hewinson, G.; Neill, S.; Skuce, R.
CS Department of Veterinary Science, Queen's University Belfast (QUB), Stoney Rd., Stormont, Belfast BT4 3SD, Northern Ireland, UK. S.Roring@qub.ac.uk
SO Journal of Clinical Microbiology, (2002) Vol. 40, No. 6, pp. 2126-2133. 35 ref.
Publisher: American Society for Microbiology (ASM). Washington
ISSN: 0095-1137
CY United States
DT Journal
LA English
ED Entered STN: 20020905
Last Updated on STN: 20020905
AB Various genetic markers have been exploited for fingerprinting the Mycobacterium ***tuberculosis*** complex (MTBC) in molecular epidemiological studies, mainly through identifying restriction fragment length polymorphisms (RFLP). In large-scale studies, RFLP typing has practical processing and analysis limitations; therefore, attempts have been made to move towards PCR-based typing techniques. Spoligotyping (spacer oligotyping) and, more recently, ***variable*** - ***number*** ***tandem*** ***repeat*** (***VNTR***) typing have provided PCR-derived typing techniques. This study describes the identification and characterization of novel ***VNTR*** loci, consisting of tandem repeats in the size range of 53 to 59 bp in the MTBC, and their assessment as typing tools in 47 M. bovis field isolates and nine MTBC strains.

Spoligotyping and the previously described set of exact tandem repeats (ETRs) were also applied to the same panel of isolates. The allelic diversity of the individual ***VNTR*** loci was calculated, and a comparison of the novel VNTRs was made against the results obtained by spoligotyping and the existing set of ETRs. Eleven unique spoligotypes were discriminated in the panel of 47 M. bovis isolates. Greater resolution was obtained through the combination of the most-discriminating VNTRs from both sets. Considerable discrimination was achieved, with the 47 M. bovis isolates resolved into 14 unique profiles, while all nine MTBC isolates were uniquely differentiated. The novel ***VNTR*** markers described increased the discrimination possible in strain typing of M. bovis, with the added benefit of an intuitive digital nomenclature, with the allele copy number of the individual VNTRs providing a profile. ***VNTR*** typing was shown to be a valuable technique with great potential for further development and application to epidemiological tracing of ***tuberculosis*** transmissions.

L8 ANSWER 87 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 20
AN 2002:426280 CAPLUS
DN 137:380514
TI ***Variable*** - ***number*** ***tandem*** ***repeat*** typing of Mycobacterium ***tuberculosis*** isolates with low copy numbers of IS6110 by using mycobacterial interspersed repetitive units
AU Cowan, Lauren Steinlein; Mosher, Laura; Diem, Lois; Massey, Jeffrey P.; Crawford, Jack T.
CS Division of AIDS, Centers for Disease Control and Prevention, Atlanta, GA, 30333, USA
SO Journal of Clinical Microbiology (2002), 40(5), 1592-1602
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB A study set of 180 Mycobacterium ***tuberculosis*** and Mycobacterium bovis isolates having low copy nos. of IS6110 were genotyped using the recently introduced method based on the variable-no. tandem repeats of mycobacterial interspersed repetitive units (MIRU- ***VNTR***). The results were compared with results of the more commonly used methods, IS6110 restriction fragment length polymorphism (RFLP) and spoligotyping. The isolates were collected in Michigan from 1996 to 1999 as part of a project to genotype all isolates from new cases of ***tuberculosis*** in the state. Twelve MIRU loci were amplified, and the amplicons were analyzed by agarose gel electrophoresis to det. the copy no. at each MIRU locus. MIRU- ***VNTR*** produced more distinct patterns (80 patterns) than did IS6110 RFLP (58 patterns), as would be expected in this study set. Spoligo-typing identified 59 patterns. No single method defined all unique isolates, and the combination of all three typing methods generated 112 distinct patterns identifying 90 unique isolates and 90 isolates in 22 clusters. The results confirm the potential utility of MIRU- ***VNTR*** typing and show that typing with multiple methods is required to attain max. specificity.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 88 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 21
AN 2003:54442 BIOSIS
DN PREV200300054442
TI Rifampin- and multidrug-resistant ***tuberculosis*** in Russian civilians and prison inmates: Dominance of the Beijing strain family.
AU Drobniewski, Francis [Reprint Author]; Balabanova, Yanina; Ruddy, Michael; Weldon, Laura; Jeltkova, Katya; Brown, Timothy; Malomanova, Nadezdna; Elizarova, Elvira; Melentyey, Alexander; Mutovkin, Ebgeny; Zhakharova, Svetlana; Fedorin, Ivan
CS Public Health Laboratory Service, Mycobacterium Reference Unit, Department of Microbiology and Infection, Guy's, King's and St Thomas' Medical School, King's College Hospital (Dulwich), East Dulwich Grove, London, SE22 8QF, UK
francis.drobniewski@kcl.ac.uk
SO Emerging Infectious Diseases, (November 2002) Vol. 8, No. 11, pp. 1320-1326. print.
ISSN: 1080-6040.

DT Article
LA English
ED Entered STN: 22 Jan 2003
Last Updated on STN: 22 Jan 2003
AB Consecutive patient cultures (140) of Mycobacterium ***tuberculosis*** were collected from five Russian civilian and prison ***tuberculosis*** laboratories and analyzed for rifampin (rpoB) and isoniazid resistance (inhA, katG, ahpC); transmission of Beijing family isolates; and the importance of prison and previous therapy in drug resistance. Rifampin, isoniazid, and multidrug resistance occurred in 58.2%, 51.6%, and 44.7% of cultures, respectively; 80% of prison cultures were rifampin resistant. Spoligotyping and ***variable*** ***number*** ***tandem*** ***repeat*** (***VNTR***) fingerprinting divided the isolates into 43 groups. Spoligotyping demonstrated that a high proportion (68.1%) of patients were infected with Beijing family strains and that most (69.1%) were rifampin resistant; the highest proportion (81.6%) occurred in prison. One ***VNTR*** subgroup (42435) comprised 68 (72.3%) of the Beijing isolates with a small number of IS6110 types; 50 (73.5%) were rifampin resistant. Rifampin-resistant Beijing isolates are dominant within the patient population, especially among prisoners, and threaten treatment programs.

L8 ANSWER 89 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:934270 CAPLUS
DN 138:52573
TI Molecular typing of Mycobacterium ***tuberculosis*** strains with a common two-band IS6110 pattern
AU Lok, Kerry H.; Benjamin, William H., Jr.; Kimerling, Michael E.; Pruitt, Virginia; Mulcahy, Donna; Robinson, Nancy; Keenan, Nancy B.; Dunlap, Nancy E.
CS University of Alabama School of Medicine, Birmingham, AL, USA
SO Emerging Infectious Diseases (2002), 8(11), 1303-1305
CODEN: EIDIFA; ISSN: 1080-6040
PB National Center for Infectious Diseases, Centers for Disease Control and Prevention
DT Journal
LA English
AB The authors conducted a program of population-based mol. typing of all Mycobacterium ***tuberculosis*** isolates obtained in Alabama since 1994. Of 2452 isolates, 1013 (41%) had fewer than 6 bands of IS6110; 348 (14%) had a single two-band pattern (JH2). With conventional epidemiol. methods, the authors identified three groups of related patients with JH2 isolates. Spoligotyping and pattern of variable no. of tandem repeats identified 10 mol. groups; two found by conventional methods were subdivided.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 90 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:949721 CAPLUS
DN 138:232257
TI Methods used in the molecular epidemiology of ***tuberculosis***
AU Mostroem, P.; Gordon, M.; Sola, C.; Ridell, M.; Rastogi, N.
CS Department of Medical Microbiology and Immunology, Goeteborg University, Goeteborg, Swed.
SO Clinical Microbiology and Infection (2002), 8(11), 694-704
CODEN: CMINFM; ISSN: 1198-743X
PB Blackwell Science Ltd.
DT Journal; General Review
LA English
AB A review on the most common and some promising new mol. methods used in epidemiol. studies of ***tuberculosis*** . The IS6110-RFLP is currently the ref. std. for typing strains of Mycobacterium ***tuberculosis*** . This method is considered as the most discriminatory and has therefore remained as the ultimate tool for identifying epidemiol. clusters.
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 91 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:195803 CAPLUS

DN 137:196184
TI Discrimination of single-copy IS6110 DNA fingerprints of Mycobacterium ***tuberculosis*** isolates by high-resolution minisatellite-based typing
AU Lee, Ann S. G.; Tang, Lynn L. H.; Lim, Irene H. K.; Bellamy, Richard; Wong, Sin-Yew
CS Department of Clinical Research, Singapore General Hospital, Singapore, 169608, Singapore
SO Journal of Clinical Microbiology (2002), 40(2), 657-659
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Seven isoniazid-resistant isolates with mutations in the NADH dehydrogenase (ndh) gene were molecularly typed by IS6110-based restriction fragment length polymorphism anal. All seven isolates with the R268H mutation had identical 1.4-kb IS6110 fingerprints. High-resoln. minisatellite-based typing discriminated five of these isolates; two isolates were identical.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 92 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 22
AN 2002:197542 BIOSIS
DN PREV200200197542
TI Discrimination of Mycobacterium ***tuberculosis*** complex bacteria using novel ***VNTR*** -PCR targets.
AU Skuce, Robin A. [Reprint author]; McCorry, Thomas P.; McCarroll, Julie F.; Roring, Solvig M. M.; Scott, Alistair N.; Brittain, David; Hughes, Stephen L.; Hewinson, R. Glyn; Neill, Sydney D.
CS Veterinary Sciences Division, Department of Agriculture and Rural Development, Stormont, Belfast, BT4 3SD, UK
Robin.Skuce@dardni.gov.uk
SO Microbiology (Reading), (February, 2002) Vol. 148, No. 2, pp. 519-528. print.
ISSN: 1350-0872.
DT Article
LA English
ED Entered STN: 13 Mar 2002
Last Updated on STN: 13 Mar 2002
AB The lack of a convenient high-resolution strain-typing method has hampered the application of molecular epidemiology to the surveillance of bacteria of the Mycobacterium ***tuberculosis*** complex, particularly the monitoring of strains of Mycobacterium bovis. With the recent availability of genome sequences for strains of the M. ***tuberculosis*** complex, novel PCR-based M. ***tuberculosis*** -typing methods have been developed, which target the variable-number tandem repeats (VNTRs) of minisatellite-like mycobacterial interspersed repetitive units (MIRUs), or exact tandem repeats (ETRs). This paper describes the identification of seven ***VNTR*** loci in M. ***tuberculosis*** H37Rv, the copy number of which varies in other strains of the M. ***tuberculosis*** complex. Six of these VNTRs were applied to a panel of 100 different M. bovis isolates, and their discrimination and correlation with spoligotyping and an established set of ETRs were assessed. The number of alleles varied from three to seven at the novel ***VNTR*** loci, which differed markedly in their discrimination index. There was positive correlation between spoligotyping, ETR- and ***VNTR*** -typing. ***VNTR*** -PCR discriminates well between M. bovis strains. Thirty-three allele profiles were identified by the novel VNTRs, 22 for the ETRs and 29 for spoligotyping. When ***VNTR*** - and ETR-typing results were combined, a total of 51 different profiles were identified. Digital nomenclature and databasing were intuitive. VNTRs were located both in intergenic regions and annotated ORFs, including PPE (novel glycine-asparigine-rich) proteins, a proposed source of antigenic variation, where VNTRs potentially code repeating amino acid motifs. ***VNTR*** -PCR is a valuable tool for strain typing and for the study of the global molecular epidemiology of the M. ***tuberculosis*** complex. The novel ***VNTR*** targets identified in this study should additionally increase the power of this approach.

L8 ANSWER 93 OF 145 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN DUPLICATE 23

AN 2002201364 EMBASE

TI Predominant ***VNTR*** family of strains of Mycobacterium ***tuberculosis*** isolated from South Asian patients.

AU Gascoyne-Binzi D.M.; Barlow R.E.L.; Essex A.; Gelletlie R.; Khan M.A.; Hafiz S.; Collyns T.A.; Frizzell R.; Hawkey P.M.

CS Dr. D.M. Gascoyne-Binzi, Department of Microbiology, General Infirmary, Great George Street, Leeds LS1 3EX, United Kingdom. deborahg@pathology.leeds.ac.uk

SO International Journal of Tuberculosis and Lung Disease, (2002) 6/6 (492-496).
Refs: 16
ISSN: 1027-3719 CODEN: IJTDFO

CY France

DT Journal; Article

FS 004 Microbiology
015 Chest Diseases, Thoracic Surgery and Tuberculosis
017 Public Health, Social Medicine and Epidemiology

LA English

SL English; French; Spanish

AB SETTING: Despite the low incidence of ***tuberculosis*** in the UK, some minority ethnic groups, particularly those originating from South Asia, experience very high incidence rates. OBJECTIVE: Comparison of the ***variable*** ***number*** ***tandem*** ***repeat*** (***VNTR***) profiles of strains of Mycobacterium ***tuberculosis*** circulating in an immigrant community in the UK with those found in the country of ethnic origin. DESIGN: Isolates of M. ***tuberculosis*** were collected from samples obtained from patients attending clinics in Leeds and Bradford, UK and Rawalpindi, Pakistan. Strains were compared using ***VNTR*** analysis and mixed-linker PCR. RESULTS: Comparison of ***VNTR*** profiles found that one profile (42235) represented 37% of patient isolates from Rawalpindi and 23% of patient isolates in Leeds and Bradford, where it was associated exclusively with patients with South Asian names. A second profile (02235) represented 15% of patient isolates in Leeds and Bradford, and was also exclusively associated with the South Asian community. These profiles could be subdivided by mixed-linker PCR analysis. CONCLUSION: The ***VNTR*** profile 42235 may represent a family of strains commonly found in communities associated with South Asia.

L8 ANSWER 94 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 2002:608976 BIOSIS

DN PREV200200608976

TI Correlations among IS6110, spoligotyping, MIRU and MLVA in the molecular epidemiology of Mycobacterium ***tuberculosis*** .

AU Spurgiesz, R. S. [Reprint author]; Smith, K. [Reprint author]; Keim, P. [Reprint author]; Steinlein, L.; Crawford, J.; Quitugua, T.; Robisin, R.; Abert, H.

CS Northern Arizona University, Flagstaff, AZ, USA

SO Abstracts of the General Meeting of the American Society for Microbiology, (2002) Vol. 102, pp. 477. print.
Meeting Info.: 102nd General Meeting of the American Society for Microbiology. Salt Lake City, UT, USA. May 19-23, 2002. American Society for Microbiology.
ISSN: 1060-2011.

DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)

LA English

ED Entered STN: 27 Nov 2002
Last Updated on STN: 27 Nov 2002

AB Mycobacterium ***tuberculosis*** extracts a tremendous cost in human lives each year worldwide. The ***tuberculosis*** epidemiology would benefit from an improvements molecular typing system. Currently, IS6110 and spoligotyping are most widely used in the typing of M. ***tuberculosis*** . More recently, MIRU (mycobacterium interspersed repetitive unit) and MLVA (Multi-locus ***variable*** ***number*** ***tandem*** ***repeat*** analysis) have shown to be rapid and reproducible methods. MLVA typing was effective across 108 isolates collected in Utah between 1995-2000. MIRU and MLVA both use PCR to

amplify various ***VNTR*** loci in the genome of M. ***tuberculosis*** . Genotype correlations amongst IS6110 and spoligotyping have been found previously. Similar associations between spoligotyping and MLVA have been found using 88 closely related strains from Texas. In this study, we analyze data from all four typing methods across 180 isolates collected throughout the United States between 1995-2000. Cluster analysis was performed for each data type individually and, then, collectively across all methods. MIRU results in combination with MLVA have comparable discrimination equivalent to the combined results of IS6110 and spoligotyping. Thus, MIRU and MLVA demonstrate a reliable, rapid, and discriminatory typing system. These ***VNTR*** methods could be an important contribution to the field of molecular epidemiology of M. ***tuberculosis*** .

L8 ANSWER 95 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:608972 BIOSIS
DN PREV200200608972
TI A Mycobactrium ***tuberculosis*** strain which is similar to CDC 1551 strain.
AU Lok, K. H. [Reprint author]; Benjamin, W. H., Jr. [Reprint author]; Kimerling, M. [Reprint author]; Dunlap, N. E. [Reprint author]
CS University of Alabama at Birmingham, Birmingham, AL, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2002) Vol. 102, pp. 476. print.
Meeting Info.: 102nd General Meeting of the American Society for Microbiology. Salt Lake City, UT, USA. May 19-23, 2002. American Society for Microbiology.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 27 Nov 2002
Last Updated on STN: 27 Nov 2002
AB Introduction: In a population based study isolates from 96% of the culture positive ***tuberculosis*** cases during the past eight years in Alabama, have been typed using multiple genetic markers. Of the 2500 strains typed one geographically localized strain, AL401-T, representing 54 cases, was found to be closely related to the strain CDC1551 (also known as the "Oshkosh" strain). Methods: Restriction Fragment Length Polymorphism (RFLP) IS6110, and Spacer Oligo typing (spoligotyping), were done according to standard methods. Variable Number of Tandem Repeats (***VNTR***) typing was performed as previously reported (Frothingham, et. al. Microbiology (1998), 144, 1189-1196). DNA sequencing was done at DNA sequencing core facility at UAB according to standard procedures. Results: Compared with CDC1551, all AL401-T isolates are sensitive to all anti-TB medications and have identical ***VNTR*** patterns 6,3,2,2,2,3,3. Four of AL401-T's five IS6110 insertion sites match those in CDC 1551 and sequencing showed the same spacers in the DR region. The spoligotype was negative for spacer 39. Both strains have a duplicated spacer 25 between spacer 31 and 32. But, because AL401-T has one extra copy of IS6110 inserted in spacer 39 in the DR region, it has a different IS6110 RFLP image than CDC1551. Both have 4 bands on IS6110 Southern blots but because AL401-T has an additional insertion in spacer 39 in the opposite orientation compared to the spacer 24 insertion, the largest CDC1551 band is truncated in AL401-T. Discussion: AL401-T is extremely common in our 2500 isolates. The majority of the members of this cluster of 56 cases is localize to a small geographic area (two-mile radius) and based on reactivation data may have been present for more than 35 years. This strain is also notable because of a very high reactivation rate (22.9%). Conclusion: By using multiple genotyping methods, we found that AL401-T, which is an extremely persistent strain in our population, is closely related to strain CDC 1551.

L8 ANSWER 96 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 24
AN 2002:303113 CAPLUS
DN 139:33139
TI Molecular characterization of multiple-drug-resistant Mycobacterium ***tuberculosis*** isolates from northwestern Russia and analysis of rifampin resistance using RNA/RNA mismatch analysis as compared to the line probe assay and sequencing of the rpoB gene
AU Mokrousov, Igor; Filliol, Ingrid; Legrand, Eric; Sola, Christophe; Otten,

Tatiana; Vyshnevskaya, Elena; Limeschenko, Elena; Vyshnevskiy, Boris; Narvskaya, Olga; Rastogi, Nalin

CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur de Guadeloupe, Pointe-a-Pitre, 97165, Guadeloupe

SO Research in Microbiology (2002), 153(4), 213-219
CODEN: RMCREW; ISSN: 0923-2508

PB Editions Scientifiques et Medicales Elsevier

DT Journal

LA English

AB This investigation evaluated the potential of RNA/RNA mismatch anal. for the detection of rifampin resistance among 38 multiple-drug-resistant (MDR) isolates of Mycobacterium ***tuberculosis*** from northwestern Russia. The results obtained were compared with a commercialized line probe assay and rpoB sequencing, and the genetic diversity of the isolates was also investigated in parallel using spoligotyping and variable no. of tandem DNA repeats (***VNTR***). The mismatch anal. revealed 3 distinct RNA cleavage profiles permitting the subdivision of the strains into mutation groups 1 to 3, the most common being group 1 (28 of 38 isolates) that contained a majority of strains with a TCG531>TTG (Ser->Leu) mutation, followed by group 2 (6 of 38 isolates) characterized by different mutations in the codon CAC526 (His), and group 3 (4 of 38 isolates), all characterized by a GAC516(Asp) mutation. Spoligotyping revealed the Beijing type to be the most prevalent among mismatch group 1 (24 out of 28 strains), suggesting that the most frequent rpoB mutation among the Beijing family in our setting was TCG531>TTG (Ser->Leu). All the Beijing type isolates were also characterized by a unique ***VNTR*** pattern made up of exact tandem repeats (ETR)-A to E of 42435. We conclude that the Beijing genotype constitutes the major family of MDR-TB isolates currently circulating in northwestern Russia, and that the inhouse RNA/RNA mismatch anal. may be successfully used for rapid and reliable diagnosis of rifampin-resistant ***tuberculosis*** in this setting.

RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 97 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 25

AN 2003:329565 BIOSIS

DN PREV200300329565

TI Molecular epidemiological manual for Mycobacterium ***tuberculosis*** complex and Mycobacterium avium using ***VNTR*** (Variable Numbers of Tandem Repeats) typing.

AU Nishimori, Kei [Reprint Author]; Uchida, Ikuo; Tanaka, Kiyoshi; Nishimori, Tomoko; Imai, Kunitoshi; Kashiwazaki, Yoshihito; Murata, Norihisa; Jinma, Kiyoe

CS Hokkaido Research Station, National Institute of Animal Health, Hitsujigaoka-4, Sapporo, Hokkaido, 062-0045, Japan
kei@affrc.go.jp

SO Bulletin of the National Institute of Animal Health, (2002) No. 109, pp. 25-32. print.
ISSN: 1347-2542 (ISSN print).

DT Article

LA Japanese

ED Entered STN: 16 Jul 2003
Last Updated on STN: 16 Jul 2003

AB In order to introduce the new molecular epidemiological analysis of Mycobacterium ***tuberculosis*** complex and Mycobacterium avium using ***VNTR*** (Variable Numbers of Tandem Repeats) typing, laboratory protocols from PCR to phylogenetic analysis are described.

L8 ANSWER 98 OF 145 USPATFULL on STN

AN 2001:214828 USPATFULL

TI Mass spectrometric detection of polypeptides

IN Little, Daniel, Boston, MA, United States
Koster, Hubert, La Jolla, CA, United States
Higgins, G. Scott, Paisley, United Kingdom
Lough, David, Berwickshire, United Kingdom

PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)

PI US 6322970 B1 20011127

AI US 1998-146054 19980902 (9)

RLI Continuation-in-part of Ser. No. US 1997-922201, filed on 2 Sep 1997

DT Utility
FS GRANTED
EXNAM Primary Examiner: Campbell, Eggerton A.
LREP Seidman, Stephanie L.Heller Ehrman White & McAuliffe LLP
CLMN Number of Claims: 95
ECL Exemplary Claim: 1
DRWN 3 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 4786
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A process for determining the identity of a target polypeptide using mass spectroscopy is provided. Depending on the target polypeptide to be identified, a process as disclosed can be used, for example, to diagnose a genetic disease or chromosomal abnormality, a predisposition to a disease or condition, or infection by a pathogenic organism; or for determining identity or heredity. Kits for performing the disclosed processes also are provided.

L8 ANSWER 99 OF 145 USPATFULL on STN
AN 2001:173357 USPATFULL
TI Polynucleotides encoding fatty acid transport proteins
IN Stahl, Andreas, Allston, MA, United States
Hirsch, David J., Brookline, MA, United States
Lodish, Harvey F., Brookline, MA, United States
Gimeno, Ruth E., Wellesley, MA, United States
Tartaglia, Louis A., Newton, MA, United States
PA Whitehead Institute for Biomedical Research, Cambridge, MA, United States (U.S. corporation)
Millennium Pharmaceuticals, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 6300096 B1 20011009
AI US 1999-232197 19990114 (9)
PRAI US 1998-71374P 19980115 (60)
US 1998-93491P 19980720 (60)
US 1998-110941P 19981204 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Stucker, Jeffrey; Assistant Examiner: Seharaseyon, Jegatheesan
LREP Hamilton, Brook, Smith & Reynolds, P.C.
CLMN Number of Claims: 66
ECL Exemplary Claim: 1
DRWN 203 Drawing Figure(s); 169 Drawing Page(s)
LN.CNT 3314
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A family of fatty acid transport proteins (FATPs) mediate transport of long chain fatty acids (LCFAs) across cell membranes into cells. These proteins exhibit different expression patterns among the organs of mammals. Nucleic acids encoding FATPs of this family, vectors comprising these nucleic acids, as well as the production of FATP proteins in host cells are described. Also described are methods to test FATPs for fatty acid transport function, and methods to identify inhibitors or enhancers of transport function. The altering of LCFA uptake by administering to the mammal an inhibitor or enhancer of FATP transport function of a FATP in the small intestine can decrease or increase calories available as fats, and can decrease or increase circulating fatty acids. The organ specificity of FATP distribution can be exploited in methods to direct drugs, diagnostic indicators and so forth to an organ such as the heart.

L8 ANSWER 100 OF 145 USPATFULL on STN
AN 2001:173337 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, La Jolla, CA, United States
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6300076 B1 20011009
AI US 2000-495444 20000131 (9)
RLI Continuation of Ser. No. US 1996-617256, filed on 18 Mar 1996, now patented, Pat. No. US 6043031 Continuation-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995, now patented, Pat. No. US 5605798
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.

LREP Seidman, Stephanie L.Heller Ehrman White & McAuliffe LLP
CLMN Number of Claims: 18
ECL Exemplary Claim: 9
DRWN 85 Drawing Figure(s); 57 Drawing Page(s)
LN.CNT 2865
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting particular nucleic acid molecules and sequences in the molecules are provided. Depending upon the sequence to be detected, the processes, for example, can be used to diagnose a genetic disease or a chromosomal abnormality, a predisposition to a disease or condition, or infection by a pathogen, or for determining identity or heredity.

L8 ANSWER 101 OF 145 USPATFULL on STN
AN 2001:153104 USPATFULL
TI Fatty acid transport proteins
IN Stahl, Andreas, Allston, MA, United States
Hirsch, David J., Brookline, MA, United States
Lodish, Harvey F., Brookline, MA, United States
Gimeno, Ruth E., Wellesley, MA, United States
Tartaglia, Louis A., Newton, MA, United States
PA Whitehead Institute for Biochemical Research, Cambridge, MA, United States (U.S. corporation)
PI US 6288213 B1 20010911
AI US 1999-232200 19990114 (9)
PRAI US 1998-71374P 19980115 (60)
US 1998-93491P 19980720 (60)
US 1998-110941P 19981204 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Kunz, Gary L.; Assistant Examiner: Hamud, Fozia
LREP Hamilton, Brook, Smith & Reynolds, P.C.
CLMN Number of Claims: 14
ECL Exemplary Claim: 1
DRWN 202 Drawing Figure(s); 169 Drawing Page(s)
LN.CNT 3180
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A family of fatty acid transport proteins (FATPs) mediate transport of long chain fatty acids (LCFAs) across cell membranes into cells. These proteins exhibit different expression patterns among the organs of mammals. Nucleic acids encoding FATPs of this family, vectors comprising these nucleic acids, as well as the production of FATP proteins in host cells are described. Also described are methods to test FATPs for fatty acid transport function, and methods to identify inhibitors or enhancers of transport function. The altering of LCFA uptake by administering to the mammal an inhibitor or enhancer of FATP transport function of a FATP in the small intestine can decrease or increase calories available as fats, and can decrease or increase circulating fatty acids. The organ specificity of FATP distribution can be exploited in methods to direct drugs, diagnostic indicators and so forth to an organ such as the heart.

L8 ANSWER 102 OF 145 USPATFULL on STN
AN 2001:147698 USPATFULL
TI Polynucleotides encoding fatty acid transport proteins
IN Stahl, Andreas, Allston, MA, United States
Hirsch, David J., Brookline, MA, United States
Lodish, Harvey F., Brookline, MA, United States
PA Whitehead Institute for Biomedical Research, Cambridge, MA, United States (U.S. corporation)
PI US 6284487 B1 20010904
AI US 1999-232191 19990114 (9)
PRAI US 1998-71374P 19980115 (60)
US 1998-93491P 19980720 (60)
US 1998-110941P 19981204 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Saoud, Christine; Assistant Examiner: Hamud, Fozia
LREP Hamilton, Brook, Smith & Reynolds, P.C.
CLMN Number of Claims: 80
ECL Exemplary Claim: 1
DRWN 57 Drawing Figure(s); 33 Drawing Page(s)

LN.CNT 2203
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A family of fatty acid transport proteins (FATPs) mediate transport of long chain fatty acids (LCFAs) across cell membranes into cells. These proteins exhibit different expression patterns among the organs of mammals. Nucleic acids encoding FATPs of this family, are described. Also described are methods to test FATPs for fatty acid transport function, and methods to identify inhibitors or enhancers of transport function. The altering of LCFA uptake by administering to the mammal an inhibitor or enhancer of FATP transport function of a FATP can decrease or increase calories available as fats, and can decrease or increase circulating fatty acids. The organ specificity of FATP distribution can be exploited in methods to direct drugs, diagnostic indicators and so forth to an organ.

L8 ANSWER 103 OF 145 USPATFULL on STN
AN 2001:136378 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, La Jolla, CA, United States
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6277573 B1 20010821
AI US 1999-287681 19990406 (9)
RLI Continuation of Ser. No. US 1996-617256, filed on 18 Mar 1996, now patented, Pat. No. US 6043031 Continuation-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995, now patented, Pat. No. US 5605798
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Seidman, Stephanie L.Heller Ehrman White & McAuliffe LLP
CLMN Number of Claims: 45
ECL Exemplary Claim: 1
DRWN 85 Drawing Figure(s); 57 Drawing Page(s)
LN.CNT 2931
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting particular nucleic acid molecules and sequences in the molecules are provided. Depending upon the sequence to be detected, the processes, for example, can be used to diagnose a genetic disease or a chromosomal abnormality, a predisposition to a disease or condition, or infection by a pathogen, or for determining identity or heredity.

L8 ANSWER 104 OF 145 USPATFULL on STN
AN 2001:121251 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, La Jolla, CA, United States
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6268144 B1 20010731
AI US 1999-397766 19990915 (9)
RLI Continuation of Ser. No. US 1996-617256, filed on 18 Mar 1996, now patented, Pat. No. US 6043031 Continuation-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995, now patented, Pat. No. US 5605798
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Seidman, Stephanie L.Heller Ehrman White & McAuliffe LLP
CLMN Number of Claims: 18
ECL Exemplary Claim: 1
DRWN 90 Drawing Figure(s); 57 Drawing Page(s)
LN.CNT 2890
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting particular nucleic acid molecules and sequences in the molecules are provided. Depending upon the sequence to be detected, the processes, for example, can be used to diagnose a genetic disease or a chromosomal abnormality, a predisposition to a disease or condition, or infection by a pathogen, or for determining identity or heredity.

L8 ANSWER 105 OF 145 USPATFULL on STN
AN 2001:107623 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, La Jolla, CA, United States

Little, Daniel P., Boston, MA, United States
Braun, Andreas, San Diego, CA, United States
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6258538 B1 20010710
AI US 1999-287679 19990406 (9)
RLI Continuation of Ser. No. US 1996-617256, filed on 18 Mar 1996, now patented, Pat. No. US 6043031 And Ser. No. US 1999-287679, filed on 6 Apr 1999 Continuation-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995, now patented, Pat. No. US 5605798 , said Ser. No. US 617256 Continuation-in-part of Ser. No. US 406199
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Seidman, Stephanie L.Heller Ehrman White & McAuliffe LLP
CLMN Number of Claims: 59
ECL Exemplary Claim: 1
DRWN 85 Drawing Figure(s); 57 Drawing Page(s)
LN.CNT 3036
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting particular nucleic acid molecules and sequences in the molecules are provided. Depending upon the sequence to be detected, the processes, for example, can be used to diagnose a genetic disease or a chromosomal abnormality, a predisposition to a disease or condition, or infection by a pathogen, or for determining identity or heredity.

L8 ANSWER 106 OF 145 USPATFULL on STN
AN 2001:75134 USPATFULL
TI Polynucleotides encoding calpain 10
IN Horikawa, Yukio, Kobe, Japan
Oda, Naohisa, Nagoya, Japan
Hanis, Craig L., Houston, TX, United States
Bell, Graeme I., Chicago, IL, United States
Cox, Nancy J., Inverness, IL, United States
PA ARCH Development Corporation & Board of Regents, Chicago, IL, United States (U.S. corporation)
The University of Texas System, Austin, TX, United States (U.S. corporation)
PI US 6235481 B1 20010522
AI US 1999-422869 19991021 (9)
PRAI US 1998-105052P 19981021 (60)
US 1999-134175P 19990513 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: Arthur, Lisa B.; Assistant Examiner: Goldberg, Jeanine
LREP Fulbright & Jaworski LLP
CLMN Number of Claims: 88
ECL Exemplary Claim: 1
DRWN 68 Drawing Figure(s); 48 Drawing Page(s)
LN.CNT 6152
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates generally to the field of diabetes. More particularly, it concerns the identification of genes responsible for NIDDM1 for use in diagnostic and therapeutic applications. The present invention demonstrates that the NIDDM1 locus is, in fact, the calpain 10 gene. The invention further relates to the discovery that analysis of mutations in calpain genes and gene products can be diagnostic for type 2 diabetes. The invention also contemplates methods of treating diabetes in view of the fact that calpain mutations can cause diabetes. Further, the invention relates to novel polynucleotides of the NIDDM1 locus and polypeptides encoded by such polynucleotides.

L8 ANSWER 107 OF 145 USPATFULL on STN
AN 2001:75131 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, La Jolla, CA, United States
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6235478 B1 20010522
AI US 1999-287682 19990406 (9)
RLI Continuation of Ser. No. US 1996-617256, filed on 18 Mar 1996, now patented, Pat. No. US 6043031 Continuation-in-part of Ser. No. US

1995-406199, filed on 17 Mar 1995, now patented, Pat. No. US 5605798
DT Utility
FS Granted
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Seidman, Stephanie L.Heller Ehrman White & McAuliffe LLP
CLMN Number of Claims: 4
ECL Exemplary Claim: 1
DRWN 85 Drawing Figure(s); 57 Drawing Page(s)
LN.CNT 2773
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting particular nucleic acid molecules and sequences in the molecules are provided. Depending upon the sequence to be detected, the processes, for example, can be used to diagnose a genetic disease or a chromosomal abnormality, a predisposition to a disease or condition, or infection by a pathogen, or for determining identity or heredity.

L8 ANSWER 108 OF 145 USPATFULL on STN
AN 2001:59628 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, La Jolla, CA, United States
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6221605 B1 20010424
AI US 2000-504245 20000215 (9)
RLI Continuation of Ser. No. US 1996-617256, filed on 18 Mar 1996, now patented, Pat. No. US 6043031 Continuation-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995, now patented, Pat. No. US 5605798
DT Utility
FS Granted
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Seidman, Stephanie L.Heller Ehrman White & McAuliffe LLP
CLMN Number of Claims: 13
ECL Exemplary Claim: 2
DRWN 85 Drawing Figure(s); 57 Drawing Page(s)
LN.CNT 2798
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting particular nucleic acid molecules and sequences in the molecules are provided. Depending upon the sequence to be detected, the processes, for example, can be used to diagnose a genetic disease or a chromosomal abnormality, a predisposition to a disease or condition, or infection by a pathogen, or for determining identity or heredity.

L8 ANSWER 109 OF 145 USPATFULL on STN
AN 2001:59624 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, La Jolla, CA, United States
Higgins, G. Scott, Glasgow, United Kingdom
Little, Daniel P., Groton, MA, United States
Braun, Andreas, San Diego, CA, United States
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6221601 B1 20010424
AI US 1999-431613 19991102 (9)
RLI Continuation of Ser. No. US 1996-617256, filed on 18 Mar 1996, now patented, Pat. No. US 6043031 Continuation-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995, now patented, Pat. No. US 5605798
DT Utility
FS Granted
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Seidman, Stephanie L.Heller Ehrman White & McAuliffe LLP
CLMN Number of Claims: 6
ECL Exemplary Claim: 1
DRWN 85 Drawing Figure(s); 57 Drawing Page(s)
LN.CNT 2839
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting particular nucleic acid molecules and sequences in the molecules are provided. Depending upon the sequence to be detected, the processes, for example, can be used to diagnose a genetic disease or a chromosomal abnormality, a predisposition to a disease or condition, or infection by a pathogen, or for determining identity or heredity.

L8 ANSWER 110 OF 145 USPATFULL on STN
AN 2001:43928 USPATFULL
TI Diagnostics based on mass spectrometric detection of translated target polypeptides
IN Little, Daniel P., La Jolla, CA, United States
Higgins, Scott, Paisley, United Kingdom
Koster, Hubert, La Jolla, CA, United States
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6207370 B1 20010327
AI US 1997-922201 19970902 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Campbell, Eggerton A.
LREP Seidman, Stephanie L.Heller Ehrman White & McAuliffe LLP
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN 2 Drawing Figure(s); 1 Drawing Page(s)
LN.CNT 1914
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides a means of detecting and identifying mutations in a genetic region, and a means of quantifying the number of repeat units in, for example, a trinucleotide repeat, by transcription/translation of the genetic region into a target polypeptide. The method requires neither radioisotopic nor fluorescent labeling of the target polypeptide. In particular, the invention is based on mass spectrometric determination of the mass of the encoded target polypeptide and comparison of the mass of the polypeptide with its own expected mass or with the mass of a polypeptide of known identity. Depending on the target polypeptide to be identified, the processes can be used, for example, to diagnose a genetic disease or chromosomal abnormality; a predisposition to a disease or condition, infection by a pathogenic organism, or for determining identity or heredity.

L8 ANSWER 111 OF 145 USPATFULL on STN
AN 2001:32995 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, La Jolla, CA, United States
PA Sequenom, Inc, San Diego, CA, United States (U.S. corporation)
PI US 6197498 B1 20010306
AI US 1999-287141 19990406 (9)
RLI Continuation of Ser. No. US 1996-617256, filed on 18 Mar 1996, now patented, Pat. No. US 6043031 Continuation-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995, now patented, Pat. No. US 5605798
DT Utility
FS Granted
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Seidman, StephanieHeller, Ehrman, White & McAuliffe LLP
CLMN Number of Claims: 45
ECL Exemplary Claim: 1
DRWN 85 Drawing Figure(s); 57 Drawing Page(s)
LN.CNT 2898
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fast and highly accurate mass spectrometry-based processes for detecting particular nucleic acid molecules and sequences in the molecules are provided. Depending upon the sequence to be detected, the processes, for example, can be used to diagnose a genetic disease or a chromosomal abnormality, a predisposition to a disease or condition, or infection by a pathogen, or for determining identity or heredity.

L8 ANSWER 112 OF 145 USPATFULL on STN
AN 2001:10718 USPATFULL
TI Antigen carbohydrate compounds and their use in immunotherapy
IN McKenzie, Ian F. C., Victoria, Australia
Apostolopoulos, Vasso, Victoria, Australia
Pietersz, Geoff Allan, Victoria, Australia
PA Austin Research Institute, Victoria, Australia (non-U.S. corporation)
PI US 6177256 B1 20010123
AI US 1998-223043 19981230 (9)
RLI Continuation of Ser. No. US 1997-833807, filed on 9 Apr 1997, now patented, Pat. No. US 5989552 Continuation of Ser. No. US 1994-340711,

filed on 16 Nov 1994, now abandoned
PRAI AU 1993-3223 19931226
DT Utility
FS Granted
EXNAM Primary Examiner: Park, Hankyel
LREP Dann Dorfman Herrell and Skillman, P.C.
CLMN Number of Claims: 16
ECL Exemplary Claim: 1
DRWN 23 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 1427
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Conjugates between one or more repeated subunits of an antigen and a carbohydrate polymer are desired. Also described are immunogenic vaccines against disease states which contain the conjugates and methods for inducing cell-mediated immune responses. The conjugates may especially contain polymers of the carbohydrate mannose and one or more repeated subunits of human mucin.

L8 ANSWER 113 OF 145 USPATFULL on STN
AN 2001:1492 USPATFULL
TI Method for eliciting Th1-specific immune response
IN Samuel, John, Edmonton, Canada
Kwon, Glen, Waunakee, WI, United States
PA University of Alberta, Edmonton, Canada (non-U.S. corporation)
PI US 6168804 B1 20010102
WO 9640066 19961219
AI US 1997-737896 19970924 (8)
WO 1996-US9951 19960607
19970924 PCT 371 date
19970924 PCT 102(e) date
RLI Continuation-in-part of Ser. No. US 1995-480499, filed on 7 Jun 1995, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Bansal, Geetha P.
LREP Fish & Richardson P.C.
CLMN Number of Claims: 13
ECL Exemplary Claim: 1,9
DRWN 38 Drawing Figure(s); 19 Drawing Page(s)
LN.CNT 1268
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method is provided for treating a Th1 mediated disease state by administration to a subject of a slow release vehicle such as a liposome or microsphere formulation containing an antigenic peptide and a Th1 specific immunomodulator wherein the antigenic peptide contains a T cell epitope and is released from the vehicle at a rate in the range from about 10 to 2 weight percent of the peptide in 24 hours at 37.degree. C.

L8 ANSWER 114 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 26
AN 2001:543083 BIOSIS
DN PREV200100543083
TI Automated high-throughput genotyping for study of global epidemiology of Mycobacterium ***tuberculosis*** based on mycobacterial interspersed repetitive units.
AU Supply, Philip [Reprint author]; Lesjean, Sarah; Savine, Evgueni; Kremer, Kristin; van Soolingen, Dick; Locht, Camille
CS Laboratoire des Mecanismes Moleculaires de la Pathogenese Bacterienne, INSERM U447, Institut Pasteur de Lille, 1, Rue du Prof. Calmette, F-59019, Lille Cedex, France
Philip.Supply@pasteur-lille.fr
SO Journal of Clinical Microbiology, (October, 2001) Vol. 39, No. 10, pp. 3563-3571. print.
CODEN: JCMIDW. ISSN: 0095-1137.
DT Article
LA English
ED Entered STN: 21 Nov 2001
Last Updated on STN: 25 Feb 2002
AB Large-scale genotyping of Mycobacterium ***tuberculosis*** is especially challenging, as the current typing methods are labor-intensive and the results are difficult to compare among laboratories. Here,

automated typing based on variable-number tandem repeats (VNTRs) of genetic elements named mycobacterial interspersed repetitive units (MIRUs) in 12 mammalian minisatellite-like loci of M. ***tuberculosis*** is presented. This system combines analysis of multiplex PCRs on a fluorescence-based DNA analyzer with computerized automation of the genotyping. Analysis of a blinded reference set of 90 strains from 38 countries (K. Kremer et al., J. Clin. Microbiol. 37:2607-2618, 1999) demonstrated that it is 100% reproducible, sensitive, and specific for M. ***tuberculosis*** complex isolates, a performance that has not been achieved by any other typing method tested in the same conditions. MIRU-VNTRs can be used for analysis of the global genetic diversity of M. ***tuberculosis*** complex strains at different levels of evolutionary divergence. To fully exploit the portability of this typing system, a website was set up for the analysis of M. ***tuberculosis*** MIRU-***VNTR*** genotypes via the Internet. This opens the way for global epidemiological surveillance of ***tuberculosis*** and should lead to novel insights into the evolutionary and population genetics of this major pathogen.

L8 ANSWER 115 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 27
AN 2001:411561 BIOSIS
DN PREV200100411561
TI Comparison of ***variable*** ***number*** ***tandem*** ***repeat*** and IS6110-restriction fragment length polymorphism analyses for discrimination of high- and low-copy-number IS6110 Mycobacterium ***tuberculosis*** isolates.
AU Barlow, Rachael E. L.; Gascoyne-Binzi, Deborah M. [Reprint author]; Gillespie, Stephen H.; Dickens, Anne; Qamer, Shabnam; Hawkey, Peter M.
CS The Division of Microbiology, Department of Microbiology, The General Infirmary, Great George Street, Leeds, LS1 3EX, UK
deborahg@pathology.leeds.ac.uk
SO Journal of Clinical Microbiology, (July, 2001) Vol. 39, No. 7, pp. 2453-2457. print.
CODEN: JCMIDW. ISSN: 0095-1137.
DT Article
LA English
ED Entered STN: 29 Aug 2001
Last Updated on STN: 22 Feb 2002
AB The present study was designed to evaluate the use of ***variable*** ***number*** ***tandem*** ***repeat*** (***VNTR***) and IS6110-restriction fragment length polymorphism (RFLP) analyses in combination as a two-step strategy for discrimination (as measured by the Hunter-Gaston Discrimination Index (HGDI)) of both high- and low-copy-number IS6110 Mycobacterium ***tuberculosis*** isolates compared to IS6110-RFLP alone with an unselected collection of isolates. Individually, IS6110-RFLP fingerprinting produced six clusters that accounted for 69% of the low-copy-number IS6110 isolates (five clusters) and 5% of the high-copy-number IS6110 isolates (one cluster). A total of 39% of all the isolates were clustered (HGDI = 0.97). ***VNTR*** analysis generated a total of 35 different ***VNTR*** allele profile sets from 93 isolates (HGDI = 0.938). Combining IS6110-RFLP analysis with ***VNTR*** analysis reduced the overall percentage of clustered isolates to 29% (HGDI = 0.988) and discriminated a further 27% of low-copy-number isolates that would have been clustered by IS6110-RFLP alone. The use of ***VNTR*** analysis as an initial typing strategy facilitates further analysis by IS6110-RFLP, and more importantly, ***VNTR*** analysis subdivides some IS6110-RFLP-defined clusters containing low- and single-copy IS6110 isolates.

L8 ANSWER 116 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 28
AN 2001:176780 BIOSIS
DN PREV200100176780
TI High-resolution minisatellite-based typing as a portable approach to global analysis of Mycobacterium ***tuberculosis*** molecular epidemiology.
AU Mazars, Edith; Lesjean, Sarah; Banuls, Anne-Laure; Gilbert, Michele; Vincent, Veronique; Gicquel, Brigitte; Tibayrenc, Michel; Locht, Camille; Supply, Philip [Reprint author]
CS Laboratoire des Mecanismes Moleculaires de la Pathogenese Bacterienne,

Institut National de la Sante et de la Recherche Medicale, U447, Institut Pasteur de Lille, 1, Rue du Prof. Calmette, F-59019, Lille Cedex, France philip.supply@pasteur-lille.fr

SO Proceedings of the National Academy of Sciences of the United States of America, (February 13, 2001) Vol. 98, No. 4, pp. 1901-1906. print. CODEN: PNASA6. ISSN: 0027-8424.

DT Article

LA English

ED Entered STN: 11 Apr 2001
Last Updated on STN: 18 Feb 2002

AB The worldwide threat of ***tuberculosis*** to human health emphasizes the need to develop novel approaches to a global epidemiological surveillance. The current standard for Mycobacterium ***tuberculosis*** typing based on IS6110 restriction fragment length polymorphism (RFLP) suffers from the difficulty of comparing data between independent laboratories. Here, we propose a high-resolution typing method based on variable number tandem repeats (VNTRs) of genetic elements named mycobacterial interspersed repetitive units (MIRUs) in 12 human minisatellite-like regions of the M. ***tuberculosis*** genome. MIRU-***VNTR*** profiles of 72 different M. ***tuberculosis*** isolates were established by PCR analysis of all 12 loci. From 2 to 8 MIRU-***VNTR*** alleles were identified in the 12 regions in these strains, which corresponds to a potential of over 16 million different combinations, yielding a resolution power close to that of IS6110-RFLP. All epidemiologically related isolates tested were perfectly clustered by MIRU- ***VNTR*** typing, indicating that the stability of these MIRU-VNTRs is adequate to track outbreak episodes. The correlation between genetic relationships inferred from MIRU- ***VNTR*** and IS6110-RFLP typing was highly significant. Compared with IS6110-RFLP, high-resolution MIRU- ***VNTR*** typing has the considerable advantages of being fast, appropriate for all M. ***tuberculosis*** isolates, including strains that have a few IS6110 copies, and permitting easy and rapid comparison of results from independent laboratories. This typing method opens the way to the construction of digital global databases for molecular epidemiology studies of M. ***tuberculosis*** .

L8 ANSWER 117 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 29

AN 2001:286580 BIOSIS

DN PREV200100286580

TI Genetic diversity of Mycobacterium ***tuberculosis*** in Sicily based on spoligotyping and variable number of tandem DNA repeats and comparison with a spoligotyping database for population-based analysis.

AU Sola, Christophe [Reprint author]; Ferdinand, Severine; Mammina, Caterina; Nastasi, Antonino; Rastogi, Nalin

CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur de Guadeloupe, Morne Jolivierе, F-97165, Pointe-a-Pitre Cedex, Guadeloupe csola@pasteur.gp

SO Journal of Clinical Microbiology, (April, 2001) Vol. 39, No. 4, pp. 1559-1565. print. CODEN: JCMIDW. ISSN: 0095-1137.

DT Article

LA English

ED Entered STN: 13 Jun 2001
Last Updated on STN: 19 Feb 2002

AB In a previous study, we proposed to associate spoligotyping and typing with the variable number of tandem DNA repeats (***VNTR***) as an alternative strategy to IS6110-restriction fragment length polymorphism (RFLP) for molecular epidemiological studies on ***tuberculosis*** . The aim of the present study was to further evaluate this PCR-based typing strategy and to describe the population structure of Mycobacterium ***tuberculosis*** in another insular setting, Sicily. A collection of 106 DNA samples from M. ***tuberculosis*** patient isolates was characterized by spoligotyping and ***VNTR*** typing. All isolates were independently genotyped by the standard IS6110-RFLP method, and clustering results between the three methods were compared. The totals for the clustered isolates were, respectively, 15, 60, and 82% by IS6110-RFLP, spoligotyping, and ***VNTR*** typing. The most frequent spoligotype included type 42 that missed spacers 21 to 24 and spacers 33 to 36 and derived types 33, 213, and 273 that, together represented as much as 26% of all isolates, whereas the Haarlem clade of strains (types

47 and 50, ***VNTR*** allele 32333) accounted for 9% of the total strains. The combination of spoligotyping and ***VNTR*** typing results reduced the number of clusters to 43% but remained superior to the level of IS6110-RFLP clustering (ca. 15%). All but one IS6110-defined cluster were identified by the combination of spoligotyping and ***VNTR*** clustering results, whereas 9 of 15 spoligotyping-defined clusters could be further subdivided by IS6110-RFLP. Reinterpretation of previous IS6110-RFLP results in the light of spoligotyping- ***VNTR*** typing results allowed us to detect an additional cluster that was previously missed. Although less discriminative than IS6110-RFLP, our results suggest that the use of the combination of spoligotyping and ***VNTR*** typing is a good screening strategy for detecting epidemiological links for the study of ***tuberculosis*** epidemiology at the molecular level.

L8 ANSWER 118 OF 145 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN DUPLICATE 30
AN 2001427812 EMBASE
TI Molecular identification of streptomycin monoresistant Mycobacterium ***tuberculosis*** related to multidrug-resistant W strain.
AU Bifani P.; Mathema B.; Campo M.; Moghazeh S.; Nivin B.; Shashkina E.; Driscoll J.; Munsiff S.S.; Frothingham R.; Kreiswirth B.N.
CS B.N. Kreiswirth, Public Hlth. Res. Inst. TB Center, New York, NY 10016, United States. barry@hri.org
SO Emerging Infectious Diseases, (2001) 7/5 (842-848).
Refs: 42
ISSN: 1080-6040 CODEN: EIDIFA
CY United States
DT Journal; Article
FS 004 Microbiology
037 Drug Literature Index
LA English
SL English
AB A distinct branch of the Mycobacterium ***tuberculosis*** W phylogenetic lineage (W14 group) has been identified and characterized by various genotyping techniques. The W14 group comprises three strain variants: W14, W23, and W26, which accounted for 26 clinical isolates from the New York City metropolitan area. The W14 group shares a unique IS6110 hybridizing banding motif as well as distinct polymorphic GC-rich repetitive sequence and ***variable*** ***number*** ***tandem*** ***repeat*** patterns. All W14 group members have high levels of streptomycin resistance. When the streptomycin resistance rpsL target gene was sequenced, all members of this strain family had an identical mutation in codon 43. Patients infected with the W14 group were primarily of non-Hispanic black origin (77%); all were US-born. Including HIV positivity, 84% of the patients had at least one known risk factor for ***tuberculosis*** .

L8 ANSWER 119 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:251637 BIOSIS
DN PREV200200251637
TI Multi-Locus ***VNTR*** analysis (MLVA) for identification and epidemiological tracking of Mycobacterium ***tuberculosis*** .
AU Spurgiesz, S. [Reprint author]; Albert, H.; Smith, K. [Reprint author]; Keys, C. [Reprint author]; Robison, R.; Keim, P. [Reprint author]
CS Northern Arizona University, Flagstaff, AZ, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2001) Vol. 101, pp. 702. print.
Meeting Info.: 101st General Meeting of the American Society for Microbiology. Orlando, FL, USA. May 20-24, 2001. American Society for Microbiology.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 24 Apr 2002
Last Updated on STN: 24 Apr 2002
AB Molecular typing as an aid for epidemiological investigations is an effective method for identifying and tracking infectious pathogens. This is somewhat problematic for Mycobacterium ***tuberculosis*** because of the high degree of monomorphism among strains. Commonly, typing is

accomplished using spoligotyping or restriction fragment polymorphisms based upon insertion element probes. An alternative approach is to use a PCR-based method that utilizes the rapidly evolving sequences: variable number tandemly repeats (VNTRs). Multiple Locus ***VNTR*** Analysis (MLVA) is capable of resolving even closely related strains. We have identified many potential ***VNTR*** loci in the M. ***tuberculosis*** genome and converted a subset into a MLVA typing system. The conversion process from potential marker loci sequences to informative markers was apprx80% successful. We have used MLVA to examine 108 clinical isolates collected in Utah; about half of which were cultured from foreign immigrants. MLVA-based genetic distances were analyzed using clustering methods to identify genetic affinities. These genetic relationships suggest possible ***tuberculosis*** transmission patterns. Future studies involving MLVA will have a greater genetic resolution and be able to handle a large number of samples.

L8 ANSWER 120 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:251625 BIOSIS
DN PREV200200251625
TI Identification and differentiation of a group of zero copy IS6110 MTB strain.
AU Lok, K. H. [Reprint author]; Benjamin, W. H. [Reprint author]; Pruitt, V.; Mulcahy, D.; Hooper, D.; Lathan, M.; Kimerling, M. [Reprint author]; Hooper, N.; Razeq, J.; Cronin, W.; Robinson, N.; Brook, N.; Dunlap, N. [Reprint author]
CS University of Alabama at Birmingham, Birmingham, AL, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2001) Vol. 101, pp. 699. print.
Meeting Info.: 101st General Meeting of the American Society for Microbiology. Orlando, FL, USA. May 20-24, 2001. American Society for Microbiology.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 24 Apr 2002
Last Updated on STN: 24 Apr 2002
AB IS6110 Restriction fragment length polymorphism (RFLP) has been used to investigate Mycobacterium ***tuberculosis*** transmission within populations since the early 1990's. However, some strains have zero copies of IS6110, which precludes the use of the standard IS6110 RFLP based genotyping. These strains are rare in most US populations and usually come from cases that originate from Southeast Asia. The zero band strains are considered a "cluster." We used other genetic markers to show that a "zero band cluster" in Maryland was not a single strain. Genotyping methods used after IS6110 RFLP failed to differentiate the isolated strains included spoligotyping according to standard methods, ***VNTR*** typing as previously reported, and total genomic AluI digestion developed in our laboratory. Six zero copy IS6110 MTB case-isolates were identified among nearly 1,500 Maryland isolates. Of the 6 cases, 3 were from Vietnam, 2 patients had the same surname. The others were one each from India, Iraq, and Liberia. None had epidemiologic links. Using additional molecular techniques we were able to show that all 6 isolates were different strains. Spoligotyping patterns of all of the zero band strains had deletions that apparently included direct repeat 24. This further confirms that these are zero copy IS6110 MTB strains since most strains have an IS6110 copy in the DR region in direct repeat 24. Of the 6 zero copy IS6110 strains that we found, 3 had the same spoligotype. By using ***VNTR*** genotyping we were able to further differentiate the strain types. Our results show that all zero copy IS6110 strains were different and came from cases that originated from various continents. Conclusion: By using multiple genotyping methods, we confirmed the identification of zero copy MTB isolates. We further demonstrated that the 6 unrelated cases had different MTB strains.

L8 ANSWER 121 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 31
AN 2001:540184 BIOSIS
DN PREV200100540184
TI Mycobacterium ***tuberculosis*** phylogeny reconstruction based on combined numerical analysis with IS1081, IS6110, ***VNTR*** , and

DR-based spoligotyping suggests the existence of two new phylogeographical clades.

AU Sola, Christophe [Reprint author]; Filliol, Ingrid; Legrand, Eric; Mokrousov, Igor; Rastogi, Nalin

CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur de Guadeloupe, Morne Joliviere, F-97165, Pointe A Pitre-Cedex, Guadeloupe csola@pasteur.gp

SO Journal of Molecular Evolution, (December, 2001) Vol. 53, No. 6, pp. 680-689. print.
CODEN: JMEVAU. ISSN: 0022-2844.

DT Article

LA English

ED Entered STN: 21 Nov 2001
Last Updated on STN: 25 Feb 2002

AB This paper deals with phylogenetic relationships among a set of 90 clinical strains representative of the worldwide diversity of the Mycobacterium ***tuberculosis*** complex (Kremer et al. 1999) using eight independent genetic markers: IS6110, IS1081, the direct repeat (DR) locus, and five variable number of tandem DNA repeat loci (***VNTR***). In a preliminary experiment, phylogenetic trees based on single markers were constructed that led to the detection of some similarities between the ***VNTR*** -based and the spoligotyping-based phylogenetic trees. In the second step, a more global phenetic approach based on pairwise comparison of strains within each typing system was used, followed by calculations of mean genetic distances based on all the eight loci and the use of the neighbor-joining algorithm for tree reconstruction. This analysis confirmed our preliminary observations and suggested the existence of at least two new phylogeographical clades of M. ***tuberculosis*** , one defined as the "East African-Indian family" (EA-I), which may find its origin on the African or Asian continents, and the other as the "Latin American and Mediterranean" (LA-M) family. The existence of these two families was also validated by an independent phylogenetic analysis of spoligotyping on a larger set of shared types (n = 252) and further corroborated by ***VNTR*** and katG-gyrA results. The potential origin of these families of bacilli is discussed based on cattle domestication and human migration history. In conclusion, the information contained in insertion sequence and repetitive DNAs may serve as a model for the phylogenetic reconstruction of the M. ***tuberculosis*** complex.

L8 ANSWER 122 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2001:718796 CAPLUS

DN 136:242697

TI Typing of Mycobacterium ***tuberculosis*** clinical isolates from Siberian Region

AU Filipenko, M. L.; Norkina, O. V.; Nikonova, A. A.; Kinsht, V. N.; Naryshkina, S. L.; Al'khovik, O. V.; Kurunov, Yu. N.; Krasnov, V. A.

CS Novosib. Inst. Bioorg. Khim., Sib. Otd. RAN, Novosibirsk, Russia

SO Doklady Akademii Nauk (2001), 379(4), 558-560
CODEN: DAKNEQ; ISSN: 0869-5652

PB MAIK Nauka

DT Journal

LA Russian

AB It was shown that Mycobacterium ***tuberculosis*** clin. isolates obtained from patients of Novosibirsk region carry a rpoB gene (531 codon) mutation and are closely related. This result should be taken into consideration upon anal. of gene mutation frequencies in this particular population.

L8 ANSWER 123 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 32

AN 2001:84388 BIOSIS

DN PREV200100084388

TI Rapid identification of laboratory contamination with Mycobacterium ***tuberculosis*** using ***variable*** ***number*** ***tandem*** ***repeat*** analysis.

AU Gascoyne-Binzi, Deborah M. [Reprint author]; Barlow, Rachael E. L.; Frothingham, Richard; Robinson, Grant; Collyns, Timothy A.; Gelletlie, Ruth; Hawkey, Peter M.

CS Department of Microbiology, General Infirmary, Great George St., Leeds, LS1 3EX, UK

deborahg@pathology.leeds.ac.uk
SO Journal of Clinical Microbiology, (January, 2001) Vol. 39, No. 1, pp. 69-74. print.
CODEN: JCMIDW. ISSN: 0095-1137.
DT Article
LA English
ED Entered STN: 14 Feb 2001
Last Updated on STN: 12 Feb 2002
AB Compared with solid media, broth-based mycobacterial culture systems have increased sensitivity but also have higher false-positive rates due to cross-contamination. Systematic strain typing is rarely undertaken because the techniques are technically demanding and the data are difficult to organize. ***Variable*** ***number*** ***tandem*** ***repeat*** (***VNTR***) analysis by PCR is rapid and reproducible. The digital profile is easily manipulated in a database. We undertook a retrospective study of Mycobacterium ***tuberculosis*** isolates collected over an 18-month period following the introduction of the BACTEC MGIT 960 system. ***VNTR*** allele profiles were determined with early positive broth cultures and entered into a database with the specimen processing date and other specimen data. We found 36 distinct ***VNTR*** profiles in cultures from 144 patients. Three common ***VNTR*** profiles accounted for 45% of true-positive cases. By combining ***VNTR*** results with specimen data, we identified nine cross-contamination incidents, six of which were previously unsuspected. These nine incidents resulted in 34 false-positive cultures for 29 patients. False-positive cultures were identified for three patients who had previously been culture positive for ***tuberculosis*** and were receiving treatment. Identification of cross-contamination incidents requires careful documentation of specimen data and good communication between clinical and laboratory staff. Automated broth culture systems should be supplemented with molecular analysis to identify cross-contamination events. ***VNTR*** analysis is reproducible and provides timely results when applied to early positive broth cultures. This method should ensure that patients are not placed on unnecessary ***tuberculosis*** therapy or that cases are not falsely identified as treatment failures. In addition, areas where existing procedures may be improved can be identified.

L8 ANSWER 124 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 33
AN 2001:84386 BIOSIS
DN PREV200100084386
TI Genetic diversity of Mycobacterium africanum clinical isolates based on IS6110-restriction fragment length polymorphism analysis, spoligotyping, and variable number of tandem DNA repeats.
AU Viana-Niero, Cristina; Gutierrez, Cristina; Sola, Christophe; Filliol, Ingrid; Boulahbal, Fadila; Vincent, Veronique; Rastogi, Nalin [Reprint author]
CS Unite Tuberculose et Mycobacteries, Institut Pasteur de Guadeloupe, Morne Jolivière, F-97165, Pointe-a-Pitre Cedex, Guadeloupe
rastogi@pasteur.gp
SO Journal of Clinical Microbiology, (January, 2001) Vol. 39, No. 1, pp. 57-65. print.
CODEN: JCMIDW. ISSN: 0095-1137.
DT Article
LA English
ED Entered STN: 14 Feb 2001
Last Updated on STN: 12 Feb 2002
AB A collection of 105 clinical isolates originally identified as Mycobacterium africanum were characterized using both phenotypic and genotyping methods. The phenotypic methods included routine determination of cultural properties and biochemical tests used to discriminate among the members of the M. ***tuberculosis*** complex, whereas genotypic characterization was based on IS6110-restriction fragment length polymorphism (IS6110-RFLP) analysis, IS1081-RFLP analysis, direct repeat-based spacer oligonucleotide typing (spoligotyping), variable number of tandem DNA repeats (***VNTR***), and the polymorphism of the oxyR, pncA, and mtp40 loci. The results obtained showed that a majority of M. africanum isolates were characterized by a specific spoligotyping pattern that was intermediate between those of M. ***tuberculosis*** and M. bovis, which do not hybridize with spacers 33 to 36 and spacers 39

to 43, respectively. A tentative M. africanum-specific spoligotyping signature appeared to be absence of spacers 8, 9, and 39. Based on spoligotyping, as well as the polymorphism of oxyR and pncA, a total of 24 isolates were excluded from the final study (19 were identified as M. ***tuberculosis*** , 2 were identified as M. canetti, and 3 were identified as M. bovis). The remaining 81 M. africanum isolates were efficiently subtyped in three distinct subtypes (A1 to A3) by IS6110-RFLP analysis and spoligotyping. The A1 and A2 subgroups were relatively more homogeneous upon spoligotyping than A3. Further analysis of the three subtypes by ***VNTR*** corroborated the highly homogeneous nature of the A2 subtype but showed significant variations for subtypes A1 and A3. A phylogenetic tree based on a selection of isolates representing the three subtypes using ***VNTR*** and spoligotyping alone or in combination confirmed the subtypes described as well as the heterogeneity of subtype A3.

L8 ANSWER 125 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:359758 BIOSIS
DN PREV200100359758
TI Development of novel ***variable*** ***number*** ***tandem*** ***repeat*** (***VNTR***) typing of Mycobacterium bovis.
AU Roring, S. [Reprint author]; Scott, A. [Reprint author]; Skuce, R. A.; Neill, S. D.
CS Department of Veterinary Science, Queens' University, Belfast, BT4 3SD, UK
SO Research in Veterinary Science, (April, 2001) Vol. 70, No. Supplement A, pp. 48. print.
Meeting Info.: 55th Annual Conference on Current Topics in Veterinary Science. Scarborough, England, UK. April 09-12, 2001. Association of Veterinary Teachers and Research Workers.
CODEN: RVTSA9. ISSN: 0034-5288.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 2 Aug 2001
Last Updated on STN: 19 Feb 2002

L8 ANSWER 126 OF 145 USPATFULL on STN
AN 2000:160809 USPATFULL
TI Lyophilized reagent for polymerase chain reaction
IN Park, Han-Oh, Taejon, Korea, Republic of
Kim, Jae-Jong, Taejon, Korea, Republic of
PA Bioneer Corporation, Choongcheongbuk-Do, Korea, Republic of (non-U.S. corporation)
PI US 6153412 20001128
AI US 1998-206656 19981207 (9)
DT Utility
FS Granted
EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Siew, Jeffrey
LREP Darby & Darby
CLMN Number of Claims: 2
ECL Exemplary Claim: 1
DRWN 13 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 483
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a lyophilized reagent for PCR which is prepared by adding a stabilizing and sedimenting agent to an aqueous reaction mixture and lyophilizing thereof. The lyophilized PCR reagent of the present invention leads to a simplification of multi-step PCR manipulation, an increase of heat stability of the reaction mixture, prevention of carry-over contamination, and improved credibility of experiments. The lyophilized PCR reagent can be applied as a kit for analysis of DNA sequence or for diagnosis of diseases, which guarantee the results of high credibility in a short period of time.

L8 ANSWER 127 OF 145 USPATFULL on STN
AN 2000:37588 USPATFULL
TI DNA diagnostics based on mass spectrometry
IN Koster, Hubert, La Jolla, CA, United States
Higgens, G. Scott, Glasgow, United Kingdom
Little, Daniel P., Boston, MA, United States
PA Sequenom, Inc., San Diego, CA, United States (U.S. corporation)

PI US 6043031 20000328
AI US 1996-617256 19960318 (8)
RLI Continuation-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995, now patented, Pat. No. US 5605798
DT Utility
FS Granted
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Seidman, Stephanie L.Heller Ehrman White & McAuliffe
CLMN Number of Claims: 46
ECL Exemplary Claim: 1
DRWN 77 Drawing Figure(s); 57 Drawing Page(s)
LN.CNT 3138
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides fast and highly accurate mass spectrometer based processes for detecting a particular nucleic acid sequence in a biological sample. Depending on the sequence to be detected, the processes can be used, for example, to diagnose a genetic disease or chromosomal abnormality; a predisposition to a disease or condition, infection by a pathogenic organism, or for determining identity or heredity.

L8 ANSWER 128 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 34
AN 2000:452706 BIOSIS
DN PREV200000452706
TI Molecular characterization of Mycobacterium ***tuberculosis*** H37Rv/Ra variants: Distinguishing the mycobacterial laboratory strain.
AU Bifani, P.; Moghazeh, S.; Shopsin, B.; Driscoll, J.; Ravikovitch, A.; Kreiswirth, B. N. [Reprint author]
CS Public Health Research Institute Tuberculosis Center, 455 First Ave., New York, NY, 10016, USA
SO Journal of Clinical Microbiology, (September, 2000) Vol. 38, No. 9, pp. 3200-3204. print.
CODEN: JCMIDW. ISSN: 0095-1137.
DT Article
LA English
ED Entered STN: 25 Oct 2000
Last Updated on STN: 10 Jan 2002
AB The Mycobacterium ***tuberculosis*** strains H37Rv and H37Ra are the most commonly used controls for M. ***tuberculosis*** identification in the clinical and research laboratory setting. To reduce the likelihood of misidentification and possible cross-contamination with this laboratory neotype, it is important to be able to distinguish H37 from clinical isolates. To provide a reference for identifying H37, we used multiple molecular techniques to characterize H37 strains, including 18 of the most frequently used variants available through the American Type Culture Collection. Isolates were genotyped using gene probes to IS6110 and IS1085. In addition, we performed polymorphic GC-rich sequence typing (PGRS), spoligotyping, determination of variable number of tandem repeats (***VNTR***), and PCR amplification of the mtp40, msx4, and mpp8 polymorphic regions. Southern hybridization with IS6110 provided the most discrimination, differentiating the 18 H37 isolates into 10 discrete patterns made up of 9 H37Rv variants and 1 H37Ra variant. PGRS, IS1085, mpp8, and spoligotyping were not able to distinguish any H37 variants, while ***VNTR*** and msx4 discriminated two. Only IS6110 and spoligotyping could distinguish the H37 strain from clinical isolates. In summary, spoligotyping and IS6110 provide a rapid and accurate way to identify H37 contamination, though IS6110 can, in addition, classify many of the H37 variants that would otherwise require phenotypic segregation.

L8 ANSWER 129 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 35
AN 2000:360661 BIOSIS
DN PREV200000360661
TI Molecular typing of Mycobacterium ***tuberculosis*** based on variable number of tandem DNA repeats used alone and in association with spoligotyping.
AU Filliol, Ingrid; Ferdinand, Severine; Negroni, Laetitia; Sola, Christophe; Rastogi, Nalin [Reprint author]
CS Unite Tuberculose et Mycobacteries, Institut Pasteur, Morne Joliviere, F-97165, Pointea-Pitre Cedex, Guadeloupe

SO Journal of Clinical Microbiology, (July, 2000) Vol. 38, No. 7, pp. 2520-2524. print.
CODEN: JCMIDW. ISSN: 0095-1137.
DT Article
LA English
ED Entered STN: 23 Aug 2000
Last Updated on STN: 8 Jan 2002
AB Fingerprinting based on variable numbers of tandem DNA repeats (***VNTR***), a recently described methodology, was evaluated for molecular typing of Mycobacterium ***tuberculosis*** in an insular setting. In this study, ***VNTR*** fingerprinting was used alone or as a second-line test in association with spoligotyping, double-repetitive-element PCR (DRE-PCR), and IS6110 restriction fragment length polymorphism (RFLP) analysis, and the discriminatory power for each method or the combination of methods was compared by calculating the Hunter-Gaston discriminative index (HGI). The results obtained showed that in 6 out of 12 (50%) cases, ***VNTR*** -defined clusters were further subdivided by spoligotyping, compared to 7 out of 18 (39%) cases where spoligotyping-defined clusters were further subdivided by ***VNTR*** . When used alone, ***VNTR*** was the least discriminatory method (HGI = 0.863). Although ***VNTR*** was significantly more discriminatory when used in association with spoligotyping (HGI = 0.982), the combination of spoligotyping and DRE-PCR (HGI = 0.992) was still the most efficient among rapid, PCR-based methodologies, giving results comparable to IS6110 RFLP analysis. Nonetheless, ***VNTR*** typing may provide additional phylogenetical information that may be helpful to trace the molecular evolution of tubercle bacilli.

L8 ANSWER 130 OF 145 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 36
AN 2000:365577 CAPLUS
DN 133:262163
TI Variable human minisatellite-like regions in the Mycobacterium ***tuberculosis*** genome
AU Supply, Philip; Mazars, Edith; Lesjean, Sarah; Vincent, Veronique; Gicquel, Brigitte; Locht, Camille
CS Laboratoire des Mecanismes Moleculaires de la Pathogenese Bacterienne, INSERM U447, Institut Pasteur de Lille, Lille, F-59019, Fr.
SO Molecular Microbiology (2000), 36(3), 762-771
CODEN: MOMIEE; ISSN: 0950-382X
PB Blackwell Science Ltd.
DT Journal
LA English
AB Mycobacterial interspersed repetitive units (MIRUs) are 40-100 bp DNA elements often found as tandem repeats and dispersed in intergenic regions of the Mycobacterium ***tuberculosis*** complex genomes. The M. ***tuberculosis*** H37Rv chromosome contains 41 MIRU loci. After polymerase chain reaction (PCR) and sequence analyses of these loci in 31 M. ***tuberculosis*** complex strains, 12 of them were found to display variations in tandem repeat copy nos. and, in most cases, sequence variations between repeat units as well. These features are reminiscent of those of certain human variable minisatellites. Of the 12 variable loci, only one was found to vary among genealogically distant BCG substrains, suggesting that these interspersed bacterial minisatellite-like structures evolve slowly in mycobacterial populations.
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 131 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2000:390899 BIOSIS
DN PREV200000390899
TI Molecular identification of streptomycin resistant Mycobacterium ***tuberculosis*** W variant cluster.
AU Bifani, J. P. [Reprint author]; Mathema, B.; Campo, M.; Moghazeh, S.; Driscoll, J.; Kreiswirth, B.
CS New York University Medical Center, New York City, NY, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2000) Vol. 100, pp. 653. print.
Meeting Info.: 100th General Meeting of the American Society for Microbiology. Los Angeles, California, USA. May 21-25, 2000. American Society for Microbiology.

ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 13 Sep 2000
Last Updated on STN: 8 Jan 2002

L8 ANSWER 132 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 37
AN 2000:314293 BIOSIS
DN PREV200000314293
TI Identification of possible loci of variable number of tandem repeats in Mycobacterium ***tuberculosis*** .
AU Smittipat, N.; Palittapongarnpim, P. [Reprint author]
CS Department of Microbiology, Faculty of Science, Mahidol University, Rama 6 Road, Bangkok, 10400, Thailand
SO Tubercle and Lung Disease, (2000) Vol. 80, No. 2, pp. 69-74. print.
CODEN: TLDIEP. ISSN: 0962-8479.
DT Article
LA English
ED Entered STN: 26 Jul 2000
Last Updated on STN: 7 Jan 2002
AB Three ***VNTR*** loci were previously cloned from Mycobacterium ***tuberculosis*** in our laboratory. The ***VNTR*** sequences were used as queries to search for similar sequences in the GenBank database by the BLAST program. Direct and tandem repeats were identified visually. The search revealed 45 more loci of direct and tandem repeats. Comparison of the sequences to the ones in the genome sequence database of the M. ***tuberculosis*** CDC1551 strain revealed 22 different loci. Combining these results with previously reported experimental work, at least 24 loci should be polymorphic enough to be detected by simple PCR. The repeats are present both inside coding sequences and in intergenic regions on the 5' or 3' ends of genes. M. ***tuberculosis*** contains several ***VNTR*** . Studies of their functions may be useful for understanding the differences of phenotypes between strains.

L8 ANSWER 133 OF 145 USPATFULL on STN
AN 1999:150655 USPATFULL
TI Antigen carbohydrate compounds and their use in immunotherapy
IN McKenzie, Ian F. C., Victoria, Australia
Pietersz, Geoff Allen, Victoria, Australia
Apostolopoulos, Vasso, Victoria, Australia
PA Austin Research Institute, Victoria, Australia (non-U.S. corporation)
PI US 5989552 19991123
AI US 1997-833807 19970409 (8)
RLI Continuation of Ser. No. US 1994-340711, filed on 16 Nov 1994, now abandoned
PRAI AU 1993-3223 19931224
DT Utility
FS Granted
EXNAM Primary Examiner: Knode, Marian C.; Assistant Examiner: Williams, Jay F.
LREP Dann, Dorfman, Herrell And Skillman
CLMN Number of Claims: 7
ECL Exemplary Claim: 1
DRWN 11 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 1551
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Conjugates between one or more repeated subunits of an antigen and a carbohydrate polymer are desired. Also described are immunogenic vaccines against disease states which contain the conjugates and methods for inducing cell-mediated immune responses. The conjugates may especially contain polymers of the carbohydrate mannose and one or more repeated subunits of human mucin.

L8 ANSWER 134 OF 145 USPATFULL on STN
AN 1999:110164 USPATFULL
TI Ligase/polymerase-mediated genetic bit analysis of single nucleotide polymorphisms and its use in genetic analysis
IN Nikiforov, Theo, Baltimore, MD, United States
Karn, Jonathan, Little Shelord, United Kingdom
Goelet, Philip, Cockeysville, MD, United States

PA Orchid Biocomputer, Inc., Princeton, NJ, United States (U.S. corporation)
PI US 5952174 19990914
AI US 1997-929101 19970915 (8)
RLI Continuation of Ser. No. US 1996-694835, filed on 9 Aug 1996, now patented, Pat. No. US 5679524 which is a continuation of Ser. No. US 1994-192631, filed on 7 Feb 1994, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Marschel, Ardin H.
LREP Auerbach, Jeffrey I., Mendelson, Elliot C.Howrey & Simon
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 4 Drawing Figure(s); 4 Drawing Page(s)
LN.CNT 1299
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method is provided for determining the identity of a nucleotide at a preselected site in a nucleic acid molecule. The method involves the incorporation of a nucleoside triphosphate that is complementary to the nucleotide present at the preselected site onto the terminus of a primer molecule, and their subsequent ligation to a second oligonucleotide. The reaction is monitored by detecting a specific label attached to the reaction's solid phase or by detection in solution.

L8 ANSWER 135 OF 145 USPATFULL on STN
AN 1999:7239 USPATFULL
TI Lyophilized reagent for polymerase chain reaction
IN Park, Han-Oh, Taejon, Korea, Republic of
Kim, Jae-Jong, Taejon, Korea, Republic of
PA Bioneer Corporation, Korea, Republic of (non-U.S. corporation)
PI US 5861251 19990119
AI US 1996-732662 19961015 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Naff, David M.; Assistant Examiner: Kerr, Janet M.
LREP Darby & Darby
CLMN Number of Claims: 2
ECL Exemplary Claim: 1
DRWN 7 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 415
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a process for preparing a ready-to-use reagent for PCR, which comprises the steps of adding the stabilizer, glucitol or glucose, to an aqueous polymerase chain reaction(PCR) mixture containing a reaction buffer, MgCl.sub.2, dNTPs, a DNA polymerase, the water soluble dye, bromophenol blue, xylene cyanole, bromocresol red or cresol red, a primer, and optionally, ddATP, ddCTP, ddGTP, or ddTTP, and then lyophilizing thereof. The ready-to-use PCR reagent of the present invention leads to a simplification of multi-step PCR manipulation, an increase of heat stability of the reaction mixture, prevention of carry-over contamination, and improved credibility of experiments. The ready-to-use PCR reagent can be applied as a kit for analysis of DNA sequence or for diagnosis of diseases.

L8 ANSWER 136 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 38
AN 1999:426746 BIOSIS
DN PREV199900426746
TI Comparison of methods based on different molecular epidemiological markers for typing of Mycobacterium ***tuberculosis*** complex strains: Interlaboratory study of discriminatory power and reproducibility.
AU Kremer, K. [Reprint author]; van Soolingen, D.; Frothingham, R.; Haas, W. H.; Hermans, P. W. M.; Martin, C.; Palittapongarnpim, P.; Plikaytis, B. B.; Riley, L. W.; Yakrus, M. A.; Musser, J. M.; van Embden, J. D. A.
CS Laboratory for Infectious Diseases and Perinatal Screening, Mycobacteria Department (pb22), National Institute of Public Health and the Environment (RIVM), 3720 BA, Bilthoven, Netherlands
SO Journal of Clinical Microbiology, (Aug., 1999) Vol. 37, No. 8, pp. 2607-2618. print.
CODEN: JCMIDW. ISSN: 0095-1137.
DT Article

LA English
ED Entered STN: 18 Oct 1999
Last Updated on STN: 18 Oct 1999
AB In this study, the currently known typing methods for Mycobacterium ***tuberculosis*** isolates were evaluated with regard to reproducibility, discrimination, and specificity. Therefore, 90 M. ***tuberculosis*** complex strains, originating from 38 countries, were tested in five restriction fragment length polymorphism (RFLP) typing methods and in seven PCR-based assays. In all methods, one or more repetitive DNA elements were targeted. The strain typing and the DNA fingerprint analysis were performed in the laboratory most experienced in the respective method. To examine intralaboratory reproducibility, blinded duplicate samples were included. The specificities of the various methods were tested by inclusion of 10 non-M. ***tuberculosis*** complex strains. All five RFLP typing methods were highly reproducible. The reliability of the PCR-based methods was highest for the mixed-linker PCR, followed by variable numbers of tandem repeat (***VNTR***) typing and spoligotyping. In contrast, the double repetitive element PCR (DRE-PCR), IS6110 inverse PCR, IS6110 ampliprinting, and arbitrarily primed PCR (APPCR) typing were found to be poorly reproducible. The 90 strains were best discriminated by IS6110 RFLP typing, yielding 84 different banding patterns, followed by mixed-linker PCR (81 patterns), APPCR (71 patterns), RFLP using the polymorphic GC-rich sequence as a probe (70 patterns), DRE-PCR (63 patterns), spoligotyping (61 patterns), and ***VNTR*** typing (56 patterns). We conclude that for epidemiological investigations, strain differentiation by IS6110 RFLP or mixed-linker PCR are the methods of choice. A strong association was found between the results of different genetic markers, indicating a clonal population structure of M. ***tuberculosis*** strains. Several separate genotype families within the M. ***tuberculosis*** complex could be recognized on the basis of the genetic markers used.

L8 ANSWER 137 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 39
AN 2000:175086 BIOSIS
DN PREV200000175086
TI Identification of a W variant outbreak of Mycobacterium ***tuberculosis*** via population-based molecular epidemiology.
AU Bifani, Pablo J.; Mathema, Barun; Liu, Zhiyuan; Moghazeh, Soraya L.; Shopsin, Bo; Tempalski, Barbara; Driscoll, Jeffrey; Frothingham, Richard; Musser, James M.; Alcabes, Philip; Kreiswirth, Barry N. [Reprint author]
CS Public Health Research Institute Tuberculosis Center, 455 First Ave, New York, NY, 10016, USA
SO JAMA (Journal of the American Medical Association), (Dec. 22-29, 1999) Vol. 282, No. 24, pp. 2321-2327. print.
CODEN: JAMAAP. ISSN: 0098-7484.
DT Article
LA English
ED Entered STN: 3 May 2000
Last Updated on STN: 4 Jan 2002
AB Context: Typing of Mycobacterium ***tuberculosis*** could provide a more sensitive means of identifying outbreaks than use of conventional surveillance techniques alone. Variants of the New York City W strain of M ***tuberculosis*** were identified in New Jersey. Objective: To describe the spread of the W family of M ***tuberculosis*** strains in New Jersey identified by molecular typing and surveillance data. Design: Population-based cross-sectional study. Setting and Subjects: All incident culture-positive ***tuberculosis*** cases reported in New Jersey from January 1996 to September 1998, for which the W family was defined by insertion sequence (IS) IS6110 DNA fingerprinting, polymorphic GC-rich repetitive sequence (PGRS) typing, spacer oligotyping (spoligotyping), and ***variable*** ***number*** ***tandem*** ***repeat*** (***VNTR***) analysis. Main Outcome Measure: Identification and characterization of W family clones supplemented by surveillance data. Results: Isolates from 1207 cases were analyzed, of which 68 isolates (6%) belonged to the W family based on IS6110 and spoligotype hybridization patterns. The IS6110 hybridization patterns or fingerprints revealed that 43 patients (designated group A) shared a unique banding motif not present in other W family isolates. Strains collected from the remaining 25 patients (designated group B), while related to W, displayed a variety of IS6110 patterns and did not share

this motif. The PGRS and ***VNTR*** typing confirmed the division of the W family into groups A and B and again showed group A strains to be closely related and group B strains to be more diverse. The demographic characteristics of individuals from groups A and B were specific and defined. Group A patients were more likely than group B patients to be US born (91% vs 24%, P<.001), black (76% vs 16%, P<.001), human immunodeficiency virus positive (40% vs 0%, P = .007), and residents of urban northeast New Jersey counties (P<.001). Patients with group B strains were primarily non-US born, of Asian descent, and more dispersed throughout New Jersey. No outbreak had been detected using conventional surveillance alone. Conclusions: The implementation of multiple molecular techniques in conjunction with surveillance data enabled us to identify a previously undetected outbreak in a defined geographical setting. The outbreak isolates comprise members of a distinct branch of the W family phylogenetic lineage. The use of molecular strain typing provides a proactive approach that may be used to initiate, and not just augment, traditional surveillance outbreak investigations.

L8 ANSWER 138 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 40
AN 1999:522260 BIOSIS
DN PREV199900522260
TI Phenotypic and genotypic characterization of Mycobacterium africanum isolates from West Africa.
AU Frothingham, Richard [Reprint author]; Strickland, Percy L.; Bretzel, Gisela; Ramaswamy, Srinivas; Musser, James M.; Williams, Diana L.
CS Durham VA Medical Center, 508 Fulton St., Building 4, Durham, NC, 27705, USA
SO Journal of Clinical Microbiology, (June, 1999) Vol. 37, No. 6, pp. 1921-1926. print.
CODEN: JCMIDW. ISSN: 0095-1137.
DT Article
LA English
ED Entered STN: 3 Dec 1999
Last Updated on STN: 3 Dec 1999
AB The Mycobacterium ***tuberculosis*** complex includes M. ***tuberculosis*** , M. bovis, M. africanum, and M. microti. Most clinical isolates are M. ***tuberculosis*** or M. bovis. These species can be distinguished by phenotypes and genotypes. However, there is no simple definition of M. africanum, and some authors question the validity of this species. We analyzed 17 human isolates from Sierra Leone, identified as M. africanum by biochemical and growth characteristics. We sequenced polymorphic genes and intergenic regions. We amplified DNA from six loci with variable numbers of tandem repeats (VNTRs) and determined the exact number of repeats at each locus in each strain. All M. africanum isolates had the ancestral CTG Leu at katG codon 463. Drug-resistant M. africanum isolates had katG and rpoB mutations similar to those found in drug-resistant M. bovis and M. ***tuberculosis*** . Fourteen Sierra Leone M. africanum isolates (designated group A) had katG codon 203 ACC Thr, also found in M. africanumT (the T indicates type strain) from Senegal. Group A isolates clustered with M. africanumT by ***VNTR*** analysis. Three M. africanum isolates (group B) had katG codon 203 ACT Thr, found in M. ***tuberculosisT*** , and clustered with M. ***tuberculosisT*** by ***VNTR*** analysis. Phenotypic identification of M. africanum yielded a heterogeneous collection of strains. Genotypic analyses identified a cluster (M. africanum group A) which included M. africanumT and was distinct from the rest of the M. ***tuberculosis*** complex. Future studies of M. africanum should include both phenotypic and genotypic analyses.

L8 ANSWER 139 OF 145 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 1999:861032 SCISEARCH
GA The Genuine Article (R) Number: 230DT
TI Evaluation of variable number tandem repeats (***VNTR***) and spoligotyping in IS6110 low copy M- ***tuberculosis*** strains.
AU Lok K (Reprint); Benjamin W H; Mulcahy D; Brook N; Kimerling M E; Dunlap N
CS UNIV ALABAMA, BIRMINGHAM, AL
CYA USA
SO AMERICAN JOURNAL OF RESPIRATORY AND CRITICAL CARE MEDICINE, (MAR 1999) Vol. 159, No. 3, Supp. [S], pp. A494-A494.

Publisher: AMER LUNG ASSOC, 1740 BROADWAY, NEW YORK, NY 10019.
ISSN: 1073-449X.
DT Conference; Journal
FS LIFE; CLIN
LA English
REC Reference Count: 0

L8 ANSWER 140 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2000:69008 BIOSIS
DN PREV200000069008
TI ***VNTR*** typing of M. ***tuberculosis*** as an epidemiological tool for the study of transmission of multi-drug resistant strains in Saudi Arabia.
AU Gilpin, C. M. [Reprint author]; Gascoyne-Binzi, D. M.; Barlow, R. E. L.; Hawkey, P. M.
CS Department of Pathology, Prince Charles Hospital, Rode Rd., Brisbane, QLD, 4032, Australia
SO Journal of Microbiological Methods, (Nov., 1999) Vol. 38, No. 3, pp. 234. print.
Meeting Info.: European Meeting on Molecular Diagnostics. Scheveningen, The Hague, Netherlands. October 13-16, 1999.
CODEN: JMIMDQ. ISSN: 0167-7012.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 9 Feb 2000
Last Updated on STN: 3 Jan 2002

L8 ANSWER 141 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2000:65867 BIOSIS
DN PREV200000065867
TI The use of ***variable*** ***number*** ***tandem*** ***repeat*** PCR for rapid identification of laboratory contamination with Mycobacterium ***tuberculosis*** .
AU Gascoyne-Binzi, D. M. [Reprint author]; Barlow, R. E. L.; Robinson, G. [Reprint author]; Collyns, T. A. [Reprint author]; Hawkey, P. M. [Reprint author]
CS Department of Microbiology, General Infirmary, Leeds, LS1 3EX, UK
SO Journal of Microbiological Methods, (Nov., 1999) Vol. 38, No. 3, pp. 233. print.
Meeting Info.: European Meeting on Molecular Diagnostics. Scheveningen, The Hague, Netherlands. October 13-16, 1999.
CODEN: JMIMDQ. ISSN: 0167-7012.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 9 Feb 2000
Last Updated on STN: 3 Jan 2002

L8 ANSWER 142 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 41
AN 1998:302130 BIOSIS
DN PREV199800302130
TI Genetic diversity in the Mycobacterium ***tuberculosis*** complex based on variable numbers of tandem DNA repeats.
AU Frothingham, Richard [Reprint author]; Meeker-O'Connell, Winifred A.
CS Dep. Med., Duke Univ. Med. Cent., Box 31080, Durham, NC 27710, USA
SO Microbiology (Reading), (May, 1998) Vol. 144, No. 5, pp. 1189-1196. print.
ISSN: 1350-0872.
DT Article
LA English
ED Entered STN: 15 Jul 1998
Last Updated on STN: 15 Jul 1998
AB Genetic loci containing variable numbers of tandem repeats (***VNTR*** loci) form the basis for human gene mapping and identification, forensic analysis and paternity testing. The variability of bacterial tandem repeats has not been systematically studied. Eleven tandem repeat loci in the M. ***tuberculosis*** genome were analysed. Five major polymorphic tandem repeat (MPTR) loci contained 15-bp repeats with substantial sequence variation in adjacent copies. Six exact tandem repeat (ETR) loci contained large DNA repeats with identical sequences in

adjacent repeats. These 11 loci were amplified in 48 strains to determine the number of tandem repeats at each locus. The strains analysed included 25 wild-type strains of M. ***tuberculosis*** , M. bovis, M. africanum and M. microti and 23 substrains of the attenuated M. bovis BCG vaccine. One of the five MPTR loci and all six ETR loci had length polymorphisms corresponding to insertions or deletions of tandem repeats. Most ETR loci were located in intergenic regions where copy number may influence expression of downstream genes. Each ETR locus had multiple alleles in the panel. Combined analysis identified 22 distinct allele profiles in 25 wild-type strains of the M. ***tuberculosis*** complex and five allele profiles in 23 M. bovis BCG substrains. Allele profiles were reproducible and stable, as demonstrated by analyses of multiple isolates of particular reference strains obtained from different laboratories. ***VNTR*** typing may be generally useful for strain differentiation and evolutionary studies in bacteria.

L8 ANSWER 143 OF 145 USPATFULL on STN
AN 97:96725 USPATFULL
TI Ligase/polymerase mediated genetic bit analysis of single nucleotide polymorphisms and its use in genetic analysis
IN Nikiforov, Theo, Baltimore, MD, United States
Karn, Jonathan, Little Shelord, United Kingdom
Goelet, Philip, Cockeysville, MD, United States
PA Molecular Tool, Inc., Baltimore, MD, United States (U.S. corporation)
PI US 5679524 19971021
AI US 1996-694835 19960809 (8)
RLI Continuation of Ser. No. US 1994-192631, filed on 7 Feb 1994, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Marschel, Ardin H.
LREP Howrey & Simon, Auerbach, Jeffrey I.
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN 4 Drawing Figure(s); 4 Drawing Page(s)
LN.CNT 1456
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method is provided for determining the identity of a nucleotide at a preselected site in a nucleic acid molecule. The method involves the incorporation of a nucleoside triphosphate that is complementary to the nucleotide present at the preselected site onto the terminus of a primer molecule, and their subsequent ligation to a second oligonucleotide. The reaction is monitored by detecting a specific label attached to the reaction's solid phase or by detection in solution.

L8 ANSWER 144 OF 145 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 97:901968 SCISEARCH
GA The Genuine Article (R) Number: YJ227
TI Variable number of tandem repeats in clinical strains of Haemophilus influenzae
AU vanBelkum A (Reprint); Scherer S; vanLeeuwen W; Willemse D; vanAlphen L; Verbrugh H
CS UNIV ROTTERDAM HOSP, DEPT BACTERIOL, DR MOLEWATERPLEIN 40, NL-3015 GD ROTTERDAM, NETHERLANDS (Reprint); UNIV AMSTERDAM, ACAD MED CTR, DEPT MED MICROBIOL, NL-1105 AZ AMSTERDAM, NETHERLANDS; UNIV MINNESOTA, SCH MED, DEPT MICROBIOL, MINNEAPOLIS, MN 55455
CYA NETHERLANDS; USA
SO INFECTION AND IMMUNITY, (DEC 1997) Vol. 65, No. 12, pp. 5017-5027. Publisher: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW, WASHINGTON, DC 20005-4171.
ISSN: 0019-9567.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 44
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB An algorithm capable of identifying short repeat motifs was developed and used to screen the whole genome sequence available for Haemophilus influenzae, since some of these repeats have been shown to affect bacterial virulence, Various di-to hexanucleotide repeats were identified, confirming and extending previous findings on the existence of

variable-number-of-tandem-repeat loci (VNTRs). Repeats with units of 7 or 8 nucleotides mere not encountered. For all of the 3- to 6-nucleotide repeats in the H. influenzae chromosome, PCR tests capable of detecting allelic polymorphisms were designed. Fourteen of 18 of the potential VNTRs were indeed highly polymorphic when different strains were screened. Two of the potential VNTRs appeared to be short and homogeneous in length; another one may be specific for the H. influenzae Rd strain only. One of the primer sets generated fingerprint-type DNA banding patterns. The various repeat types differed with respect to intrinsic stability as well, It was noted for separate colonies derived from a single clinical specimen or strains passaged for several weeks on chocolate agar plates that the lengths of the VNTRs did not change. When several strains from different patients infected during an outbreak of lung disease were analyzed, increased but limited variation was encountered in all ***VNTR*** sites analyzed, One of the 5-nucleotide VNTRs proved to be hypervariable, This variability may reflect the molecular basis of a mechanism used by H. influenzae bacteria to successfully colonize and infect different human individuals.

L8 ANSWER 145 OF 145 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:284867 BIOSIS
DN PREV199799584070
TI Differentiation of Mycobacterium ***tuberculosis*** complex strains by ***variable*** ***number*** ***tandem*** ***repeat*** (***VNTR***) typing.
AU Meeker-O'Connell, Winifred A. [Reprint author]; Frothingham, Richard
CS VA Med. Cent., Durham, NC, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (1997) Vol. 97, No. 0, pp. 571.
Meeting Info.: 97th General Meeting of the American Society for Microbiology. Miami Beach, Florida, USA. May 4-8, 1997.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 3 Jul 1997
Last Updated on STN: 3 Jul 1997